

SEARCH REQUEST FORM

119108

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 4/19/00
Searcher: 222
Terminal time: _____
Elapsed time: 10:420
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

☒ STIC
☐ CM-1
☐ Pre-S

Type of Search

☐ N.A. Sequence
☒ A.A. Sequence
☐ Structure
☐ Bibliographic

Vendors

☐ IG
☐ STN
☐ Dialog
☐ APS
☐ Geninfo
☐ SDC
☐ DARC/Questel
☒ Other

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 17:03:02 ; Search time 17.8804 Seconds
(without alignments)
1264.231 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242

Sequence: 1 MTVLAPAWSPTTVLLILL...RPGEQVPVPSPQDLLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	I38440	flt3 ligand - huma
2	864.5	69.6	245	S43293	FLT3/FLK2 ligand (
3	834	67.1	178	I39076	FLT3 ligand alter
4	768.5	61.9	231	A49265	flt3/flk-2 ligand
5	606.5	48.8	220	S43291	FLT3/FLK2 ligand (
6	606.5	48.8	220	I58343	flt3 ligand isofor
7	93	7.5	1217	T22672	hypothetical prote
8	92	7.4	661	T19512	74k alpha trans-in
9	89.5	7.2	474	T19543	hypothetical prote
10	89	7.2	387	I48201	adrenin - golden h
11	89	7.2	793	S60735	splicing factor SF
12	88.5	7.1	238	A81990	hypothetical prote
13	88.5	7.1	1386	T00257	hypothetical prote
14	88	7.1	753	J00532	OP protein - Kenne
15	87.5	7.0	479	A32290	protein-tyrosine-p
16	87	7.0	910	A33137	tyrosine kinase re
17	86.5	7.0	590	A40437	glutamic acid-rich
18	86	6.9	299	T17832	hypothetical prote
19	86	6.9	485	A33647	sulfated surface g
20	86	6.9	746	T28004	hypothetical prote
21	85	6.8	289	A87646	hypothetical prote
22	85	6.8	366	A37374	Fc gamma (IgG) rec
23	84	6.8	263	T03162	tegument protein 6
24	84	6.8	757	A32883	gamma-glutamyl car
25	83.5	6.7	199	E75630	hypothetical prote
26	83.5	6.7	530	A45690	transactivator EBN
27	83	6.7	1509	T19486	hypothetical prote
28	82.5	6.6	418	T19800	hypothetical prote
29	82.5	6.6	426	I36948	Ig epsilon-chain -

RESULT 1

I38440

flt3 ligand - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence revision 29-May-1998 #text_change 01-Dec-2000

C:Accession: I38440; I39075; S43292

R:Lyman, S.D.; James, L.; Johnson, L.; Braesel, K.; de Vries, P.; Escobar, S.S.; Downey,

Blood 83, 2795-2801, 1994

A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor for

A:Reference number: I38440; MUID:94235842; PMID:8180375

A:Accession: I38440

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-235 <RES>

A:Cross-references: EMBL:U03858; NID:9494978; PIDN:AAA19825.1; PID:9494979

R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, P.; Johnson, L.; Escobar, S.

Oncogene 11, 1165-1172, 1995

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032581; PMID:7566977

A:Accession: I39075

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 <RES>

A:Cross-references: EMBL:U29874; NID:91072036; PIDN:AAA30949.1; PID:91072037

R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; K

felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik,

Nature 368, 843-848, 1994

A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoiet

A:Reference number: S43290; MUID:94195428; PMID:8145851

A:Accession: S43292

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-71, 'A', 73-235 <HAN>

A:Cross-references: GB:U04806; NID:9483844; PIDN:AAA17999.1; PID:9483845

A:Note: the authors translated the codon AGT for residue 25 as Met

C:Genetics:

A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 100.0%; Score 1242; DB 2; Length 235;

Best Local Similarity 100.0%; Pred. No. 5e-99; 0; Indels 0; Gaps 0;

Matches 235; Conservative 0; Mismatches 0;

Qy 1 MTVLAPAWSPTTVLLILLSSGLSGTQCSCFQHSPISSDFAVKIRELSDYLLQDYPTV 60

Db 1 MTVLAPAWSPTTVLLILLSSGLSGTQCSCFQHSPISSDFAVKIRELSDYLLQDYPTV 60

Qy 61 ASNLQDEELCGGLRWLVLAQRWNERLKTVAGSKMQLLVRNTEIHFTVKCAFQPPPSCL 120

Db 61 ASNLQDEELCGGLRWLVLAQRWNERLKTVAGSKMQLLVRNTEIHFTVKCAFQPPPSCL 120

Qy 121 RFVQTNISRLQTSLSQVALKPWITRONFSPRCLEIQCQPDSTLPPMSPRPLETAPT 180

Db 121 RFVQTNISRLLOETSEQLVALKPWITRONFSCLELQCCPDSSTLPFPWSPRPLEATAPT 180
Qy 181 APQPPLLLLLLPVGLLLAAAWCLHWQTRRRTRPRGQVPPVPSODLLLVH 235
Db 181 APQPPLLLLLLPVGLLLAAAWCLHWQTRRRTRPRGQVPPVPSODLLLVH 235

RESULT 2
S43293
FLT3/FLK2 ligand (clone S109) - human
C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43293
R:Lyman, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; K
felt, A.; Muench, M.; Kelnar, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43293
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-245 <HAN>
A>Note: the authors translated the codon AGT for residue 25 as Met

Query Match 69.6%; Score 864.5; DB 2; Length 245;
Best Local Similarity 73.0%; Pred. No. 1.1e-66;
Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3;

Qy 1 MTVLAPAWSPPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
Db 1 MTVLAPAWSPPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60

Qy 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120

Qy 121 RFVQTNISRLLOETSEQLVALKPWITRONFSCLELQCCPDSSTLPFPWSPRPLEATAPT 180
Db 121 RFVQTNISRLLOETSEQLVALKPWITRONFSCLELQCCPDSSTLPFPWSPRPLEATAPT 180

Qy 181 APQPPLLLLLLPVGLLLAAAWCLHWQTRRRTRPRGQVPPVPSODLLLVH 235
Db 181 APQPPLLLLLLPVGLLLAAAWCLHWQTRRRTRPRGQVPPVPSODLLLVH 235

RESULT 3
I39076
FLT3 ligand alternatively spliced isoform - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I39076
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I39076
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-178 <RES>
A:Cross-references: EMBL:U29874; NID:G1072036; PIDN:AAA90950.1; PID:G1072038
C:Genetics:
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1
A:Note: the authors translated the codon AGT for residue 25 as Met

Query Match 67.1%; Score 834; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.2e-64;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTVLAPAWSPPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
Db 1 MTVLAPAWSPPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60

Db 1 MTVLAPAWSPPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
Qy 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120

Qy 121 RFVQTNISRLLOETSEQLVALKPWITRONFSCLELQCCPDSSTLPFPWSPRPLEATAPT 180
Db 121 RFVQTNISRLLOETSEQLVALKPWITRONFSCLELQCCPDSSTLPFPWSPRPLEATAPT 180

RESULT 4
A49265
flt3/flk-2 ligand precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: A49265; I49347; I49346; S43290
R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Hollir
D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a f
A:Reference number: A49265; MUID:94084791; PMID:7505204
A:Accession: A49265
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-231 <LYM>
A:Cross-references: GB:I23636; NID:G439441; PIDN:AAA9436.1; PID:G439442
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I49347
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-163, 'G', '165', 'HYAG' <RES>
A:Cross-references: EMBL:U29875; NID:G1072039; PIDN:AAA90952.1; PID:G1072041
A:Accession: I49346
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197, 'L', '198-231' <RE2>
A:Cross-references: EMBL:U29875; NID:G1072039; PIDN:AAA90951.1; PID:G1072040
R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; K
felt, A.; Muench, M.; Kelnar, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoiet
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43290
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197, 'L', '198-231' <HAN>
A:Experimental source: clone T110
A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-Va
C:Genetics:
A:Introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
C:Keywords: transmembrane protein

Query Match 61.9%; Score 768.5; DB 2; Length 231;
Best Local Similarity 70.3%; Pred. No. 1.7e-58;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

Qy 1 MTVLAPAWSPPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
Db 1 MTVLAPAWSPPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59

Qy 60 VASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 119
Db 61 VAVNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120

Qy 120 LRFVQTNISRLLOETSEQLVALKPWITRONFSCLELQCCPDSSTLPFPWSPRPLEAT 177
Db 121 LRFVQTNISRLLOETSEQLVALKPWITRONFSCLELQCCPDSSTLPFPWSPRPLEAT 180

Qy 178 APTAQPP--ILLLLLPVGLLLAAAWCLHWQTRRRTRPRGQVPPVPS 227

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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:59:26 ; Search time 12.7717 Seconds
(without alignments)

958.091 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242

Sequence: 1 MTLAPAWSPPTVLLLLLLL.....RPGEQVPVPFQDILLVH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1 FL3L HUMAN	P49772 homo sapien
2	768	61.8	232	1 FL3L MOUSE	P49772 mus musculus
3	92	7.4	661	1 AT12 V2VD	P09264 varicella-z
4	90.5	7.3	5120	1 PCLO CHICK	O9pu36 gallus gall
5	89.5	7.2	941	1 GBR2 HUMAN	O75899 homo sapien
6	89	7.2	387	1 SCGA MESAU	Q64255 mesocricetu
7	89	7.2	793	1 S3A1 HUMAN	Q15459 homo sapien
8	87.5	7.0	415	1 TNR3 MOUSE	P50284 mus musculus
9	87.5	7.0	479	1 MP1P DROME	P20483 drosophila
10	87	7.0	910	1 DDRI RAT	Q63474 rattus norv
11	87	7.0	911	1 DDRI MOUSE	Q03146 mus musculus
12	86.5	7.0	1394	1 CNG4 BOVIN	Q28181 bos taurus
13	86	6.9	485	1 SSGP VOLCA	P21937 volvox cart
14	85	6.8	282	1 ATFS HUMAN	Q9y2d1 homo sapien
15	85	6.8	366	1 FCGN RAT	P13599 rattus norv
16	84.5	6.8	3726	1 ABF1 MOUSE	Q61329 mus musculus
17	84	6.8	582	1 MNT HUMAN	O99583 homo sapien
18	84	6.8	732	1 EAL5 HUMAN	Q9hcm4 homo sapien
19	84	6.8	1234	1 NPHN RAT	Q9r044 rattus norv
20	83.5	6.7	671	1 Z282 HUMAN	Q9udv7 homo sapien
21	83	6.7	758	1 VKGG HUMAN	P38435 homo sapien
22	83	6.7	866	1 BAL MOUSE	Q8cas9 mus musculus
23	82.5	6.6	334	1 BC12 HUMAN	Q9hb09 homo sapien
24	82.5	6.6	598	1 LTB2 HUMAN	Q8n423 h leukocyte
25	82	6.6	2167	1 SHK1 RAT	Q9wv48 rattus norv
26	81.5	6.6	488	1 NM11 HUMAN	P24347 homo sapien
27	81.5	6.6	591	1 MNT MOUSE	Q08789 mus musculus
28	81.5	6.6	2212	1 T230 HUMAN	Q93074 homo sapien
29	81	6.5	283	1 ATFS MOUSE	O70191 mus musculus
30	81	6.5	387	1 SCGA MOUSE	P82350 mus musculus
31	81	6.5	428	1 EPC HUMAN	P01854 homo sapien
32	81	6.5	1248	1 DIA1 HUMAN	O60610 homo sapien
33	80.5	6.5	1402	1 IF4G_RABIT	P41110 cryptotolagus

ALIGNMENTS

RESULT 1

FL3L_HUMAN	STANDARD;	PRT;	235 AA.
ID	FL3L_HUMAN	STANDARD;	PRT;
AC	P49771;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3L).		
GN	FLT3LG.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94195428; PubMed=8145851;		
RA	Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bazaan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J., Duda G., Martina N., Peterson D., Menon S., Shanafelt A., Muench M., Keiner G., Namikawa R., Rennick D., Roncarolo M.G., Zlotnik A., Roest O., Dubreuil P., Birbaumer D., Lee F., et al. "Cloning of the human homologue of the murine Flt3 ligand: a growth factor for early hematopoietic progenitor cells." Blood 83:2795-2801(1994).		
RL	Nature 368:643-648(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94235842; PubMed=8180375;		
RA	Lyman S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S., Downey H., Splett R.K., Beckmann M.P., McKenna H.J.; "Cloning of the human homologue of the murine Flt3 ligand: a growth factor for early hematopoietic progenitor cells." Blood 83:2795-2801(1994).		
RL	Nature 368:643-648(1994).		
RN	[3]		
RP	SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.		
RX	MEDLINE=96032581; PubMed=7566977;		
RA	Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S.; "Structural analysis of human and murine Flt3 ligand genomic loci." Oncogene 11:1165-1172(1995).		
RL			
RN	[4]		
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).		
RX	MEDLINE=20343011; PubMed=10881197;		
RA	Savvides S.N., Boone T., Karplus P.A.; "Flt3 ligand structure and unexpected commonalities of helical bundles and cysteine knots." Nat. Struct. Biol. 7:486-491(2000).		
RL			
CC	-!- FUNCTION: Stimulates the proliferation of early hematopoietic cells. Synergizes well with a number of other colony stimulating factors and interleukins.		
CC	-!- SUBUNIT: Homodimer (isoform 2).		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1). Secreted (isoform 2).		
CC	-!- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2; Name=1; Synonyms=Membrane-bound;		

34	80	6.4	397	1	CEPD STRCL	P18549 streptomyc
35	80	6.4	940	1	GBR2 RAT	O88871 rattus norv
36	80	6.4	1174	1	KPC1 COCHE	O42632 cochliobolu
37	80	6.4	1427	1	ZRH2 HUMAN	Q9c0a1 homo sapien
38	80	6.4	1794	1	YDC9 SCHPO	Q10172 schizosacch
39	79.5	6.4	653	1	PCF1 MOUSE	Q64213 mus musculu
40	79.5	6.4	5085	1	PCLO RAT	Q91k66 rattus norv
41	79	6.4	805	1	KIP3 YEAST	P53086 saccharomyc
42	78.5	6.3	251	1	HXB4 HUMAN	P17483 homo sapien
43	78.5	6.3	382	1	AVRB RAT	P38445 rattus norv
44	78.5	6.3	387	1	SCGA RABIT	Q28686 cryptotolagus
45	78.5	6.3	401	1	P661 RAT	Q9qza2 rattus norv

RESULT 4
PCLO_CHICK STANDARD; PRT; 5120 AA.
AC Q9PU36; 2343 2343 POLY-PRO.
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Piccolo protein (Aczonin) (Fragment).
GN PCLO OR ACZ.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99439764; PubMed=10508862;
RA Wang X., Kibschull M., Jauze M.M., Lichte B., Petrasch-Parwez E.,
RA Killmann M.W.;
RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
RT zones, shares homology regions with rim and bassoon and binds
RT profilin.";
RL J. Cell Biol. 147:151-162(1999).
CC -!- FUNCTION: May act as a scaffolding protein involved in the
CC organization of synaptic active zones and in synaptic vesicle
CC trafficking (By similarity).
CC -!- SUBUNIT: Interacts with Rabac1/Pral and profilin (By similarity).
CC -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
CC synaptic junctions (By similarity).
CC -!- DOMAIN: C2 domain 1 is involved in binding calcium and
CC phospholipids. Calcium binds with low affinity but with high
CC specificity and induces a large conformational change.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Y19187; CAB60725.1; --
CC HSPSP; P04410; I.A25.
CC GO; GO:0045202; C:synaptic junction; ISS.
CC GO; GO:0005509; F:calcium ion binding; ISS.
CC GO; GO:0005544; F:calcium-dependent phospholipid binding; ISS.
CC GO; GO:0005522; F:profilin binding; ISS.
CC GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
CC GO; GO:0016080; P:synaptic vesicle targeting; ISS.
CC InterPro; IPR000008; C2.
CC InterPro; IPR001478; PDZ.
CC InterPro; IPR001565; Synaptotagmin.
CC InterPro; IPR008899; Znf_piccolo.
CC Pfam; PF00168; C2; 2.
CC Pfam; PF00595; PDZ; 1.
CC Pfam; PF05715; Zf_piccolo; 2.
CC PRINTS; PR00399; SYNAPTOTAGMIN.
CC SMART; SM00239; C2; 2.
CC SMART; SM00228; PDZ; 1.
CC PROSITE; PS00499; C2_DOMAIN_1; 1.
CC PROSITE; PS00004; C2_DOMAIN_2; 2.
CC PROSITE; PS0106; PDZ; 1.
CC Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
KW Repeat.
FT NON_TER 1 1
FT DOMAIN 258 357 10 X 10 AA TANDEM APPROXIMATE REPEATS OF
FT P-A-K-P-Q-P-Q-P-X.
FT ZN_FING 368 392 C4-TYPE (POTENTIAL).
FT ZN_FING 836 859 C4-TYPE (POTENTIAL).
FT

FT DOMAIN 2324 2343 2343 POLY-PRO.
FT DOMAIN 4414 4493 PDZ.
FT DOMAIN 4627 4726 C2 DOMAIN 1.
FT DOMAIN 5003 5094 C2 DOMAIN 2.
SQ SEQUENCE 5120 AA; 560751 MW; A658D9891B65B412 CRC64;
Query Match 7.3%; Score 90.5; DB 1; Length 5120;
Best Local Similarity 24.3%; Pred.No.48;
Matches 45; Conservative 19; Mismatches 72; Indels 49; Gaps 7;
Qy 90 AGSKMOGLLERVNTTEIHF-----VTKAFQPPSPCLRFVQTN----- 126
Db 2224 AARKKSTVETGIKIHEDSHKELSLDMTRINLTGATSEQPLCLCVASVSKPEASETPA 2283
Qy 127 --ISRLLQETSE-QLVALKPWITRONF-----SECLQLQCPDSSLTLPBWSPRELEATAP 179
Db 2284 VPTFRVVKSTSTVMPSSPALTSKVFSLFRSSLSLSPAQSPSPSPPPPPPPPLPPP 2343
Qy 180 TAQPQ-----PLLLLLLLFVGLLLAAWCLH-WQTRRRRRPRGEQV 221
Db 2344 ILKPAIYPKKKSIQAPMATAFTAVPLVTSVATLSSAALKHVVVTKYTFPT-PPV 2402
Qy 222 PPVPS 226
Db 2403 PPKPS 2407
RESULT 5
GBR2_HUMAN STANDARD; PRT; 941 AA.
ID GBR2_HUMAN 075974; 075975; Q8W04; Q9P1R2; Q9UNR1; Q9UN99;
AC 075999; 075974; 075975; Q8W04; Q9P1R2; Q9UNR1; Q9UN99;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Gamma-aminobutyric acid type B receptor, subunit 2 precursor (GABA-B
DE receptor 2) (GABA-B-R2) (Gb2) (GABAR2) (G protein-coupled receptor
DE 51) (GPR 51) (HG20).
GN GPR51 OR GABR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
RT GABA(B) receptor.";
RL Nature 396:679-682(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX Liu M., Parker R., McCrear K., Watson J., Baker E., Sutherland G.,
RA Herzog H.;
RT "Cloning and characterization of a novel human GABA-B receptor subtype
RT with high affinity for GABA and low affinity for baclofen.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Hippocampus;
RA Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Fetal brain;
RN

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OM protein - protein search, using sw model

Run on: April 8, 2004, 17:02:32 ; Search time 45.9783 Seconds

(without alignments)
1612.649 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242

Sequence: 1 MTVLAPAWSPPTVYLLLLLLL.....RPGQVPVPSPQDLLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvrius:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1145.5	92.2	236	6	Q865Z3 papio cynoc
2	895.5	72.1	294	6	Q9MZV0 cynmzv0 canis faml
3	894.5	72.0	291	6	Q9MZU9 cynmzu9 felis silve
4	840	67.6	292	6	Q9GKE0 cynge0 bos taurus
5	835	67.2	292	6	Q8WNW1 cynwnw1 bos taurus
6	745	60.1	274	6	Q9GKD9 cyngd9 bos taurus
7	602.5	48.5	172	11	Q61104 mus musc
8	578	46.5	169	11	Q8VCH4 mus musc
9	276	22.2	54	4	Q7Z6N5 Q7Z6N5 homo sapien
10	112.5	9.1	579	10	Q91LGG8 Q91gg8 oryza sativ
11	110	8.9	219	16	Q8DKL7 Q8dkl7 synchococc
12	105	8.5	208	10	Q8L418 Q8l418 oryza sativ
13	100.5	8.1	1809	11	Q8VIM6 Q8vim6 mus musc
14	97.5	7.9	669	10	Q8GYA4 Q8gya4 arabidopsis
15	96	7.7	474	16	Q7WSA9 Q7wsa9 bordetella
16	96	7.7	474	16	Q7VU97 Q7vu97 bordetella

17	95.5	7.7	439	4	Q8N775	Q8n775 homo sapien
18	95.5	7.7	658	10	Q8H785	Q8h785 arabidopsis
19	95.5	7.7	1240	12	Q9DWH8	Q9dwh8 rat cytomeg
20	93.5	7.5	658	10	Q9CST0	Q9cst0 arabidopsis
21	93	7.5	1217	5	Q17889	Q17889 caenorhabdi
22	92.5	7.4	387	11	Q8VD70	Q8vdd70 mus musculu
23	92.5	7.4	1400	5	Q9VDD2	Q9vdd2 drosophila
24	92	7.4	251	4	Q9HAD2	Q9had2 homo sapien
25	91.5	7.4	287	16	Q8DHH3	Q8dhh3 synchococc
26	91.5	7.4	308	11	Q8BP15	Q8bp15 mus musculu
27	91.5	7.4	674	11	Q8K4C2	Q8k4c2 mus musculu
28	89.5	7.2	474	5	Q17610	Q17610 caenorhabdi
29	88.5	7.1	238	16	Q8YWX3	Q8ywx3 anabaena sp
30	88.5	7.1	270	4	Q9UMT1	Q9umt1 homo sapien
31	88.5	7.1	356	2	Q8KR32	Q8kr32 yersinia ps
32	88.5	7.1	404	10	Q9AMJ4	Q9awj4 oryza sativ
33	88.5	7.1	579	4	Q8N158	Q8n158 homo sapien
34	88.5	7.1	1267	10	Q943D5	Q943d5 oryza sativ
35	88.5	7.1	1386	4	Q75064	Q75064 homo sapien
36	88	7.1	250	6	Q9GKE2	Q9gke2 sus scrofa
37	88	7.1	753	12	Q56971	Q56971 kennedya ye
38	88	7.1	791	11	Q8K4Z5	Q8k4z5 mus musculu
39	88	7.1	791	11	Q8C175	Q8c175 mus musculu
40	88	7.1	791	11	Q8C128	Q8c128 mus musculu
41	88	7.1	791	11	Q8COM7	Q8com7 mus musculu
42	88	7.1	815	10	Q7XPC0	Q7xpc0 oryza sativ
43	87.5	7.0	470	10	Q9LUI1	Q9lui1 arabidopsis
44	87.5	7.0	564	10	Q8L729	Q8l729 spinacia ol
45	87.5	7.0	946	10	Q22015	Q22015 cylindrothe

ALIGNMENTS

RESULT 1

Q865Z3	PRELIMINARY;	PRT;	236 AA.
ID	Q865Z3		
AC	Q865Z3;		
DT	01-JUN-2003 (TrenbLrel. 24, Created)		
DT	01-JUN-2003 (TrenbLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TrenbLrel. 25, Last annotation update)		
DE	FLT3 ligand.		
OS	Papio cynocephalus x Papio anubis.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;		
OC	Cercopitheciniae; Papio.		
OX	NCBI_TaxID=208510;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kalina T., Storek J.;		
RT	"T-cell reconstitution after autologous CD34 cell transplantation in monkeys."		
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY226585; AA072538.1; -		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0005125; F:cytokine activity; IEA.		
DR	InterPro; IPR004213; Flt3 lig.		
DR	Pfam; PF02947; flt3 lig. I.		
SQ	SEQUENCE 236 AA; 26591 MW; 740P33A6A6DC2163 CRC64;		

Query Match	92.2%;	Score 1145.5;	DB 6;	Length 236;
Best Local Similarity	94.9%;	Pred. No. 7.9e-104;		
Matches 224;	Conservative 0;	Mismatches 11;	Indels 1;	Gaps 1;
Qy	1	MTVLAPAWSPPTVYLLLLLLLSSGLSGTQDCSFQHSPTSSDFAVKIRELSYLLQDPVTV	60	
Dd	1	MTVLAPAWSPPTVYLLLLLLLSSGLSGTQDCSFQHSPTSSDFAVKIRELSYLLQDPVTV	60	
Qy	61	ASNLQDEELCGGLNRLVLAQRWMLKTVAGSKVQGLLERNVTEHFVTKCAFQPPPSCL	120	
Dd	61	PSNLQDEELCGGLNRLVLAQRWMLKTVAGSKVQGLLERNVTEHFVTKCAFQPPPSCL	120	
Qy	121	RFVQTNISRLIQETSEQLVALKPWITQNFSCRLQCCQPSSTLPPPPWSRPLEATAPT	180	


```
Db 121 RVQTNISLQETSEQLVAKPWITRQNFSGCLELQCPDSSTLPPRSPGAEALT 180
Qy 181 APQPP-LLLLLLPVGLLLAAACLHWQRTTTPRPGEOVPVPSQDILLVYEH 235
Db 181 AFQRP-LLLLLLPVGLLLAAACLHWQRTTTPRPREQVPVPSQDILLVYEH 236

RESULT 2
Q9MZV0 PRELIMINARY; PRT; 294 AA.
AC Q9MZV0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Flt3 ligand.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20358731; PubMed=10902925;
RA Yang S., Sim G.K.;
RT "Molecular cloning of canine and feline flt3 ligand reveals high
RT degree of similarity to the human and mouse homologue but uniquely
RT long cytoplasmic domain.";
RL DNA Seq. 11:163-166(2000).
DR EMBL; AF155148; AAF87088.1; -.
DR HSSP; P49771; IETE.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR InterPro; IPR004213; Flt3 lig.
DR Pfam; PF02947; flt3 lig; I.
SQ SEQUENCE 294 AA; 32394 MW; 6859917AJB74ABCD CRC64;

Query Match 72.1%; Score 895.5; DB 6; Length 294;
Best Local Similarity 77.1%; Pred. No. 2.8e-79;
Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;

Qy 1 MVLAPAWSPTTYLLLLSSGLSGTDCSFQSHSPISDFAVKIRELSYLLQDPVTV 60
Db 1 MVLAPAWSPTASLLLLSSGLSGTDCSFQSHSPISSTFAVIRKLSYLLQDPVTV 60
Qy 61 ASNLQDEELCGGLRWLVLAQRWMLKTVAGSKMOGLLERYNTEIHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGAFWLVLAQRWMLKTVAGSKMOGLLEAVNTEIHFVTKCAFQPPPSCL 120
Qy 121 RVQTNISLQETSEQLVAKPWITRQNFSGCLELQCPDSSTLPPRSPGAEALT 180
Db 121 RVQTNISHLQDTSQQAALKPWITRNFSGCLELQCPDSSTLPPRSPGAEALT 180
Qy 181 APQPP-LLLLLLPVGLLLAAACLHWQRTTTPRPGEOVPVPS- - - - - PQD 229
Db 181 AFQAPRLLLLLLPVGLLLAAACLHWQRTTTPRPGEOVPVPS- - - - - PED 236

RESULT 3
Q9MZU9 PRELIMINARY; PRT; 291 AA.
AC Q9MZU9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Flt3 ligand.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20358731; PubMed=10902925;
RA Yang S., Sim G.K.;
```

```
RT "Molecular cloning of canine and feline flt3 ligand reveals high
RT degree of similarity to the human and mouse homologue but uniquely
RT long cytoplasmic domain.";
RL DNA Seq. 11:163-166(2000).
DR EMBL; AF155149; AAF87089.1; -.
DR HSSP; P49771; IETE.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR InterPro; IPR004213; Flt3 lig.
DR Pfam; PF02947; flt3 lig; I.
SQ SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DCC6 CRC64;

Query Match 72.0%; Score 894.5; DB 6; Length 291;
Best Local Similarity 80.5%; Pred. No. 3.5e-79;
Matches 178; Conservative 9; Mismatches 33; Indels 1; Gaps 1;

Qy 1 MVLAPAWSPTTYLLLLSSGLSGTDCSFQSHSPISDFAVKIRELSYLLQDPVTV 60
Db 1 MVLAPAWSPTTSLLLSSGLSGTDCSFQSHSPISSTFKVIRKLSYLLQDPVTV 60
Qy 61 ASNLQDEELCGGLRWLVLAQRWMLKTVAGSKMOGLLERYNTEIHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGPFWLVLAQRWMLKTVAGSKMOGLLEAVNTEIHFVTKCAFQPPPSCL 120
Qy 121 RVQTNISLQETSEQLVAKPWITRQNFSGCLELQCPDSSTLPPRSPGAEALT 180
Db 121 RVQTNISHLQDTSQQAALKPWITRNFSGCLELQCPDSSTLPPRSPGAEALT 180
Qy 181 APQPP-LLLLLLPVGLLLAAACLHWQRTTTPRPGEO 220
Db 181 APOAPLLLLLLLPVGLLLAAACLHWQRTTTPRPGEO 221

RESULT 4
Q9GKE0 PRELIMINARY; PRT; 292 AA.
ID Q9GKE0
AC Q9GKE0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Flt3 ligand isoform-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20570936; PubMed=11120823;
RA Wang W., Brown W.C., Palmer G.H.;
RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms.";
RL J. Immunol. 165:6966-6974(2000).
DR EMBL; AF282985; AAF99322.1; -.
DR HSSP; P49771; IETE.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR InterPro; IPR004213; Flt3 lig.
DR Pfam; PF02947; flt3 lig; I.
SQ SEQUENCE 292 AA; 32390 MW; D68B9ED79221202D CRC64;

Query Match 67.6%; Score 840; DB 6; Length 292;
Best Local Similarity 76.3%; Pred. No. 7.5e-74;
Matches 171; Conservative 12; Mismatches 37; Indels 4; Gaps 2;

Qy 1 MVLAPAWSPTTYLLLLSSGLSGTDCSFQSHSPISDFAVKIRELSYLLQDPVTV 59
Db 1 MVLAPAWSPTTSLLLSSGLSGTDCSFQSHSPISSTFAIKIGLSYLLQDPVTV 60
Qy 60 VASNLQDEELCGGLRWLVLAQRWMLKTVAGSKMOGLLERYNTEIHFVTKCAFQPPPSCL 119
Db 61 VASNLQDQLCGAFWLVLAQRWMLKTVAGSEKLELDYNTTEIHFVTSYCAFQPPPSCL 120
```

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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:58:41 ; Search time 64.4973 Seconds
(without alignments)
1029.480 Million cell updates/sec

Title: US-08-994-468-6
Perfect score: 1242
Sequence: 1 MVLAPAWSPPTLYLLLLLL.....RPGQVPPVPQDLVLVH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	2 AAR67541	Aar67541 Human flt
2	1242	100.0	235	2 AAW67769	Aaw67769 Human flt
3	1242	100.0	235	3 AAY69719	Aay69719 Full leng
4	1242	100.0	235	4 AAB20192	Aab20192 Human Flt
5	1242	100.0	235	5 ABB08129	Abb08129 Human Flt
6	1242	100.0	235	5 ABG31626	Abg31626 Human Flt
7	1242	100.0	235	5 AAO19091	Aao19091 C neoform
8	1242	100.0	235	6 AAG79949	Aag79949 Secreted
9	1242	100.0	235	6 ABG74239	Abg74239 Human Flt
10	1242	100.0	235	7 ADD22874	Add22874 Human flt
11	1242	100.0	235	7 ADD80915	Add80915 Amino aci
12	1242	100.0	235	7 ADE48117	Ade48117 Human Flt
13	1242	100.0	235	7 ADE80752	Ade80752 Microate
14	1237	99.6	235	6 AAG79950	Aag79950 Secreted
15	1236	99.5	235	4 AAB20194	Aab20194 Human S86
16	1236	99.5	235	4 AAB20194	Aab20194 Human Flt
17	1124	90.5	212	3 AAY69721	Aay69721 Human flt
18	1114	89.7	209	2 AAW69007	Aaw69007 Human flt
19	1114	89.7	209	3 AAY69720	Aay69720 Mature wi
20	1110	89.4	209	3 AAY69729	Aay69729 Human flt
21	1110	89.4	209	3 AAY69727	Aay69727 Human flt
22	1110	89.4	209	3 AAY69723	Aay69723 Human flt
23	1110	89.4	209	3 AAY69726	Aay69726 Human flt
24	1108	89.2	209	3 AAY69722	Aay69722 Human flt
25	1108	89.2	209	3 AAY69724	Aay69724 Human flt

26	1107	89.1	209	3 AAY69728	Aay69728 Human flt
27	1100	88.6	209	3 AAY69725	Aay69725 Human flt
28	970	78.1	185	4 AAB20195	Aab20195 Human Flt
29	963	77.5	189	6 AAG79948	Aag79948 Secreted
30	895.5	72.1	294	3 AAY58204	Aay58204 Canine Fl
31	894.5	72.0	291	3 AAY58210	Aay58210 Canine Fl
32	834	67.1	178	4 AAB20193	Aab20193 Human Flt
33	822	66.2	156	6 ABP72857	Abp72857 Human flt
34	797.5	64.2	288	3 AAY58206	Aay58206 Canine ma
35	796.5	64.1	276	3 AAY58207	Aay58207 Canine Fl
36	791.5	63.7	265	3 AAY58211	Aay58211 Canine ma
37	768.5	61.9	231	2 AAR67540	Aar67540 Mouse flt
38	768.5	61.9	231	2 AAW67768	Aaw67768 Murine flt
39	768.5	61.9	231	4 AAB20186	Aab20186 Mouse flt
40	768.5	61.9	231	6 ABG74238	Abg74238 Mouse flt
41	768.5	61.9	231	7 ADD22870	Add22870 Murine flt
42	768.5	61.9	231	7 ADE48118	Ade48118 Mouse flt
43	768	61.8	232	2 AAR66177	Aar66177 Mouse M0T
44	764	61.5	232	4 AAB20189	Aab20189 Mouse flt
45	745	60.0	150	2 AAW77930	Aaw77930 Flt3 liga

ALIGNMENTS

RESULT 1
AAR67541
ID AAR67541 standard; protein; 235 AA.
XX

AC AAR67541;

XX

DT 25-MAR-2003 (revised)

DT 05-AUG-1995 (first entry)

XX Human flt-3 ligand.

XX Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.

XX Homo sapiens.

XX Key

FT Peptide

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

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FT Domain

FT Domain

FT Domain

PT and various cancers.
 PS Disclosure; Page 29-30; 33pp; English.
 XX A human T-cell lambda-gt10 random primed cDNA library was screened with a
 CC fragment corresponding to the extracellular domain of mouse flt3 ligand
 CC (flt3-L) (nt 103-516 of AAQ79076) to isolate human flt3-L cDNA. flt3-L
 CC stimulates progenitor and stem cells, and can be used e.g. in gene
 CC therapy protocols. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 235 AA;
 Query Match 100.0%; Score 1242; DB 2; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5, 8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAMPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
 DB 1 MTVLAPAMPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
 QY 61 ASNLQDEBELCGGLMRLVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 DB 61 ASNLQDEBELCGGLMRLVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVAKPWITRONFNRCLQLCQPDSSSTLPPWSPRPLEATPT 180
 DB 121 RFVQTNISRLQETSEQLVAKPWITRONFNRCLQLCQPDSSSTLPPWSPRPLEATPT 180
 QY 181 APQPPLLLLLLPGVLLLLAAWCLHWQTRTRTPRPGEQVPPVSPQDLLLLVEH 235
 DB 181 APQPPLLLLLLPGVLLLLAAWCLHWQTRTRTPRPGEQVPPVSPQDLLLLVEH 235
 RESULT 2
 AAQ67769
 ID AAQ67769 standard; protein; 235 AA.
 AC AAQ67769;
 DT 25-MAR-1999 (first entry)
 XX Human flt3-Ligand.
 DE
 XX Antigen-specific peripheral immune tolerance; flt3-Ligand; flt3-L;
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;
 KW tissue transplantation.
 XX
 OS Homo sapiens.
 XX WO9857655-A1.
 XX 23-DEC-1998.
 XX 12-JUN-1998; 98WO-US012085.
 XX 17-JUN-1997; 97US-00877421.
 XX (IMMV) IMMUNEX CORP.
 XX Abbott NM, Mowat AM, Viney JL;
 XX WPI; 1999-070422/06.
 XX N-PSDB; AAQ61506.
 XX Methods for initiating or enhancing antigen specific immune tolerance -
 PT by using murine or human flt3 ligand.
 XX Claim 1; Page 14-15; 25pp; English.
 XX A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before, after or with
 CC the mucosal administration of an immunotolerising amount of the antigen

CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino acids
 CC 28-y of human flt3-L, where y is an amino acid between 160-235; and c) a
 CC polypeptide that has at least 90% identity to the polypeptides of either
 CC (a) or (b). The method ameliorates the effects of autoimmune diseases,
 CC food allergies or organ or tissue rejection following transplantation.
 CC Administration of flt3-L allows lower doses of antigens to be used in
 CC vivo for mucosally administered antigens. The present sequence represents
 CC human flt3-L
 XX
 SQ Sequence 235 AA;
 Query Match 100.0%; Score 1242; DB 2; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5, 8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAMPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
 DB 1 MTVLAPAMPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
 QY 61 ASNLQDEBELCGGLMRLVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 DB 61 ASNLQDEBELCGGLMRLVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVAKPWITRONFNRCLQLCQPDSSSTLPPWSPRPLEATPT 180
 DB 121 RFVQTNISRLQETSEQLVAKPWITRONFNRCLQLCQPDSSSTLPPWSPRPLEATPT 180
 QY 181 APQPPLLLLLLPGVLLLLAAWCLHWQTRTRTPRPGEQVPPVSPQDLLLLVEH 235
 DB 181 APQPPLLLLLLPGVLLLLAAWCLHWQTRTRTPRPGEQVPPVSPQDLLLLVEH 235
 RESULT 3
 AAY69719
 ID AAY69719 standard; protein; 235 AA.
 AC AAY69719;
 DT 05-JUL-2000 (first entry)
 XX Full length wild type human flt-3 protein.
 DE
 XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 XX
 OS Homo sapiens.
 XX WO200001823-A2.
 XX 13-JAN-2000.
 XX 25-JUN-1999; 99WO-US014296.
 XX 02-JUL-1998; 98US-00109100.
 XX (IMMV) IMMUNEX CORP.
 XX Graddis TJ, McGrew JT;
 XX WPI; 2000-182115/16.
 XX N-PSDB; AAQ59064.
 XX Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune
 PT response stimulation or treatment of pathological conditions contains
 PT amino acid substitutions at positions 8, 84, 118 or 122.

PS Claim 1; Page 72-73; 90pp; English.

XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to the
 CC full length wild type (this sequence) or mature (AAY69720) flt3-L
 CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-L protein can be used to induce cellular
 CC expansion (especially in vivo) or differentiation, e.g. in hematopoietic,
 CC natural killer (NK) or dendritic cells, especially in the presence of
 CC growth factors such as interleukins, colony stimulating factors or
 CC protein kinases. The protein can also modulate, augment or enhance a
 CC patient's immune response and can be used to treat an immune disorder
 CC (e.g. allergy, autoimmunity or immunosuppression). The protein may be
 CC used to treat a pathological condition e.g. myelodysplasia, aplastic
 CC anemia, HIV infection, breast, small cell lung, testicular or ovarian
 CC cancer, lymphoma, multiple myeloma, neuroblastoma or acute leukemia
 XX

SQ Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 3; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLSSLSGLSGTQDCSPHSPISDFAVKIRELSYLLQDPVTV 60
 DB 1 MTVLAPAWSPTTYLLLLSSLSGLSGTQDCSPHSPISDFAVKIRELSYLLQDPVTV 60

QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKWQGLLERNVTEHFVTKCAFQPPPSCL 120
 DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKWQGLLERNVTEHFVTKCAFQPPPSCL 120

QY 121 RFVQTNISRLQETSEQLVALKPWITRQNFSCRLELQCPDSTLPPPPSPPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRQNFSCRLELQCPDSTLPPPPSPPLEATAPT 180

QY 181 APQPPLLLLLLPVGLLLAAACWLFHWQTRRRTPRPGEQVPPVPSQDILLVEH 235
 DB 181 APQPPLLLLLLPVGLLLAAACWLFHWQTRRRTPRPGEQVPPVPSQDILLVEH 235

RESULT 4
 AAB20192
 ID AAB20192 standard; protein; 235 AA.

AC AAB20192;
 XX
 XX 14-MAY-2001 (first entry)
 DT
 XX Human Flt-3 ligand.
 DE
 XX Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine; immunotherapy;
 KW therapy; tumour; cancer; melanoma; glioma; lymphoma; autoimmune disease;
 KW infection; gene therapy.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..26
 FT Protein /label= Signal_peptide
 FT Protein 27..235
 FT Protein /label= Mature_protein
 FT Domain 27..182
 FT Domain /label= Extracellular_domain
 FT Domain 183..205
 FT Domain /label= Transmembrane_domain
 FT Domain 206..235
 FT Domain /label= Cytoplasmic_domain

WO200109303-A2.
 XX
 XX 08-FEB-2001.
 PD
 XX

PF 31-JUL-2000; 200WO-US020679.
 XX
 PR 30-JUL-1999; 99US-0146170P.
 XX
 PA (VICA-) VICAL INC.
 XX
 XX Hermanson GG;
 XX
 XX WPI; 2001-123319/13.
 DR N-PSDB; AAF30310.
 XX

Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide
 and one or more antigen, or cytokine encoding polynucleotides, useful for
 suppressing tumor growth and for treating autoimmune diseases (e.g.
 rheumatoid arthritis).

Claim 2; Page 132-133; 149pp; English.

XX The present sequence is that of human Fms-like tyrosine kinase (Flt-3
 CC ligand). The invention is directed to enhancing the immune response of a
 CC vertebrate to an antigen or a cytokine by administering in vivo, into a
 CC tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or
 CC more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-
 CC encoding polynucleotide may encode the present full-length human Flt-3
 CC ligand polypeptide, or amino acids 27-180, 1-160, 27-185, 1-185, or 27-
 CC 235 of the ligand. The polynucleotides are incorporated into the cells of
 CC the vertebrate in vivo, and a prophylactically or therapeutically
 CC effective amount of Flt-3 ligand and 1 or more antigens or cytokines is
 CC produced in vivo. Pharmaceutical compositions comprising the
 CC polynucleotides are useful for suppressing tumour growth in a mammal. The
 CC tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma.
 CC They can also be used for the prophylactic and/or therapeutic treatment
 CC of: (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and
 CC C in humans), parasitic (e.g. malaria) and fungal infections; (b)
 CC autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c)
 CC cancer; and (d) Aujeszky's disease in pigs. Various other examples of
 CC these diseases are given in the specification
 XX

SQ Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 4; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLSSLSGLSGTQDCSPHSPISDFAVKIRELSYLLQDPVTV 60
 DB 1 MTVLAPAWSPTTYLLLLSSLSGLSGTQDCSPHSPISDFAVKIRELSYLLQDPVTV 60

QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKWQGLLERNVTEHFVTKCAFQPPPSCL 120
 DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKWQGLLERNVTEHFVTKCAFQPPPSCL 120

QY 121 RFVQTNISRLQETSEQLVALKPWITRQNFSCRLELQCPDSTLPPPPSPPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRQNFSCRLELQCPDSTLPPPPSPPLEATAPT 180

QY 181 APQPPLLLLLLPVGLLLAAACWLFHWQTRRRTPRPGEQVPPVPSQDILLVEH 235
 DB 181 APQPPLLLLLLPVGLLLAAACWLFHWQTRRRTPRPGEQVPPVPSQDILLVEH 235

RESULT 5
 ABB08129
 ID ABB08129 standard; protein; 235 AA.

XX
 XX ABB08129;
 AC
 XX 10-SEP-2002 (first entry)
 DT
 XX Human Flt3L polypeptide.
 XX
 XX Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
 KW fungicide; protozoicide; virucide; anti-inflammatory; anti-HIV;
 KW

KW tuberculostatic; cytostatic; human; Flt3L.
 XX Homo sapiens.
 XX WO200236141-A2.
 XX 10-MAY-2002.
 XX 30-OCT-2001; 2001WO-US044834.
 XX 02-NOV-2000; 2000US-0245721P.
 XX (IMMV) IMMUNEX CORP.
 XX Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;
 PI Thomas EK;
 XX WPI; 2002-500114/53.
 XX Treating an individual suffering from infection, e.g. inflammation,
 PT chickenpox or AIDS, by administering a combination of dendritic cell
 PT mobilization factor or maturation agent, T cell enhancing factor and
 PT antigen-specific T cells.
 XX Disclosure; Page 37-38; 43pp; English.
 XX The invention relates to treating an individual at risk for or suffering
 CC from infection with a pathogenic or opportunistic organism. The method
 CC involves administering a combination of two to five agents comprising:
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
 CC or (e) activated, antigen-specific T cells. The methods are useful for
 CC treating an individual at risk for or suffering from infection with a
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
 CC T. cruzi, which causes Chaga's disease). The methods are especially
 CC useful for treating an individual suffering from immunosuppression by
 CC enhancing a lymphocyte-mediated immune response. In particular, the
 CC method is useful for treating inflammations, chickenpox, oral or genital
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T
 CC cell leukemia or T cell lymphoma. The activated antigen-presenting
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence
 CC represents a human Flt3L polypeptide fragment, that can be used as a
 CC dendritic cell mobilisation factor
 XX SQ Sequence 235 AA;
 Query Match 100.0%; Score 1242; DB 5; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 Db 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 QY 61 ASNLODEELCGGLWRLVLAQRWMLKTVAGSKMQGLLERVNTIHFVTKCAFQPPPSCL 120
 Db 61 ASNLODEELCGGLWRLVLAQRWMLKTVAGSKMQGLLERVNTIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLLOETSEQLVALKPMITRQNFSCRLELCQCPDSSTLPPWSPRLEATPT 180
 Db 121 RFVQTNISRLLOETSEQLVALKPMITRQNFSCRLELCQCPDSSTLPPWSPRLEATPT 180
 QY 181 APQPLLLLLLLPVGLLLLLAAWCLHWORTRRTRPRGEQVPVPSQDILLVHEH 235
 Db 181 APQPLLLLLLLPVGLLLLLAAWCLHWORTRRTRPRGEQVPVPSQDILLVHEH 235
 RESULT 6
 ABG31626
 ID ABG31626 standard; protein; 235 AA.
 XX
 AC ABG31626;

29-NOV-2002 (first entry)
 Human Flt3L protein.
 Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;
 dendritic cell maturation agent; T cell enhancing factor; skin cancer;
 antigen-specific T cell; prostate cancer; liver cancer; bone tumour;
 brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;
 actinic keratosis; dendritic cell maturation stimulator; cytostatic;
 dendritic cell activator; T cell enhancer; human; Flt3L.
 Homo sapiens.
 WO200266044-A2.
 29-AUG-2002.
 23-OCT-2001; 2001WO-US046254.
 24-OCT-2000; 2000US-0242868P.
 (IMMV) IMMUNEX CORP.
 Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;
 WPI; 2002-674891/72.
 Treating an individual with tumors or cancers, e.g. liver cancer or brain
 tumor, by administering a combination of dendritic cell populations, T
 cell enhancing factors and activated, antigen-specific T cells.
 Disclosure; Page 38-39; 44pp; English.
 The present invention relates to a new method for treating a tumour-
 bearing subject. The method involves administering a combination of 2 to
 5 agents comprising dendritic cell mobilisation factor, dendritic cell
 maturation agent, tumour-killing agent, T cell enhancing factor or
 activated, antigen-specific T cells. The method is useful for treating
 tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver
 cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or
 cervical intraepithelial neoplasia. The present amino acid sequence
 represents the human Flt3L protein that was used in the method of the
 invention
 XX SQ Sequence 235 AA;
 Query Match 100.0%; Score 1242; DB 5; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 Db 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 QY 61 ASNLODEELCGGLWRLVLAQRWMLKTVAGSKMQGLLERVNTIHFVTKCAFQPPPSCL 120
 Db 61 ASNLODEELCGGLWRLVLAQRWMLKTVAGSKMQGLLERVNTIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLLOETSEQLVALKPMITRQNFSCRLELCQCPDSSTLPPWSPRLEATPT 180
 Db 121 RFVQTNISRLLOETSEQLVALKPMITRQNFSCRLELCQCPDSSTLPPWSPRLEATPT 180
 QY 181 APQPLLLLLLLPVGLLLLLAAWCLHWORTRRTRPRGEQVPVPSQDILLVHEH 235
 Db 181 APQPLLLLLLLPVGLLLLLAAWCLHWORTRRTRPRGEQVPVPSQDILLVHEH 235
 RESULT 7
 AAO19091
 ID AAO19091 standard; protein; 235 AA.
 XX
 AC AAO19091;

XX DT 22-NOV-2002 (first entry)

XX C neoformans antigen expressing dendritic cell related protein #1.

DE Human; fungicide; fungal infection; dendritic cell; antigen;

KW Cryptococcus neoformans; vaccine; immunostimulant.

XX Homo sapiens.

XX WO200266053-A2.

XX 29-AUG-2002.

XX 14-DEC-2001; 2001WO-US048288.

XX 04-JAN-2001; 2001US-0259653P.

XX (IMMV) IMMUNEX CORP.

XX Thomas EK;

XX WPI; 2002-674896/72.

XX Producing a population of activated, Cryptococcus neoformans antigen-presenting dendritic cells for preventing or treating C. neoformans infection comprises causing the obtained dendritic cells to present the antigen.

XX Disclosure; Page 25-26; 32pp; English.

XX The present invention relates to a method of producing a population of activated, Cryptococcus neoformans antigen-presenting dendritic cells, comprising causing the obtained dendritic cells to present the antigen and maturing the dendritic cells. The activated, C. neoformans antigen-expressing dendritic cells are useful for treating, or as vaccines or vaccine adjuvants against, C. neoformans infection, or for generating C. neoformans-specific T cells. The present sequence is a human protein shown in the exemplification of the invention

XX SQ Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 5; Length 235;

Best Local Similarity 100.0%; Pred. No. 5.8e-109;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLPAWSPTTYILLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

DB 1 MTVLPAWSPTTYILLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEIHFTVKAFQPPPSCL 120

DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEIHFTVKAFQPPPSCL 120

QY 121 RFVQTNISRLLOETSEQLVAKPWITRONFSRCLQCPDSSSTLPPWSPRPLEATAPT 180

DB 121 RFVQTNISRLLOETSEQLVAKPWITRONFSRCLQCPDSSSTLPPWSPRPLEATAPT 180

QY 181 APQPLLLLLLPVGLLLAAAWCLHWQTRTRTPRPGEQVPPVPSQDILLVEH 235

DB 181 APQPLLLLLLPVGLLLAAAWCLHWQTRTRTPRPGEQVPPVPSQDILLVEH 235

RESULT 8

AAG79949

ID AAG79949 standard; protein; 235 AA.

XX AAG79949;

XX 23-OCT-2003 (revised)

DT 16-MAY-2003 (first entry)

XX Secreted human protein comparison protein #1.

XX Gene; secreted; tyrosine kinase receptor ligand; subfamily; phosphorylation; kidney; blood; lung; brain glioblastoma; prostate; colon; leukocyte.

XX unidentified.

XX WO2003002138-A1.

XX 09-JAN-2003.

XX 25-JUN-2002; 2002WO-US020172.

XX 27-JUN-2001; 2001US-00891498.

XX (PEKE) PE CORP NY.

XX Gong F, Ceccardi T, Ladunga I;

XX WPI; 2003-267895/26.

XX New isolated human secreted peptide and nucleic acids, useful for the development of human therapeutics and diagnostic compositions, drug screening assays, tissue typing and pharmacogenomic analysis.

XX Disclosure; Fig 2A; 66pp; English.

XX The sequences given in AAG79949-50 are included in the scope of the invention as they show high levels of similarity to the secreted peptide of the invention. The secreted protein is related to the tyrosine kinase receptor ligand subfamily. This protein effects protein phosphorylation. The human secreted peptides are useful in substantial and specific assays related to functional information of the peptide sequences, to raise antibodies or to elicit immune response, as reagents in assays that determine the levels of protein in biological fluids, and as markers for tissues where the corresponding protein is expressed. The peptides and the antibodies are useful in drug screening assays, tissue typing and pharmacogenomic analysis. The nucleic acid molecules are useful as probes, primers and chemical intermediates in biological assays, for constructing recombinant vectors, and expressing antigenic portions of the protein. The peptide and nucleic acid molecules are useful in the identification of therapeutic proteins and may serve as models or targets for the development of human therapeutic agents that modulate human secreted peptide activity in cells and tissues that express the secreted peptide, such as in kidney, blood, lung, brain glioblastomas, prostate, colon or leukocytes. (Updated on 23-OCT-2003 to standardise OS field)

XX SQ Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 6; Length 235;

Best Local Similarity 100.0%; Pred. No. 5.8e-109;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLPAWSPTTYILLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

DB 1 MTVLPAWSPTTYILLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEIHFTVKAFQPPPSCL 120

DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEIHFTVKAFQPPPSCL 120

QY 121 RFVQTNISRLLOETSEQLVAKPWITRONFSRCLQCPDSSSTLPPWSPRPLEATAPT 180

DB 121 RFVQTNISRLLOETSEQLVAKPWITRONFSRCLQCPDSSSTLPPWSPRPLEATAPT 180

QY 181 APQPLLLLLLPVGLLLAAAWCLHWQTRTRTPRPGEQVPPVPSQDILLVEH 235

DB 181 APQPLLLLLLPVGLLLAAAWCLHWQTRTRTPRPGEQVPPVPSQDILLVEH 235

RESULT 9

ABG74239

ID ABG74239 standard; protein; 235 AA.

XX AC ABG74239;
 XX DT 16-APR-2003 (first entry)
 XX DE Human Flt-3 ligand, Flt-3 L.
 XX KW Human; flt-3 ligand; flt-3 L; stem cell disorder; cancer; cytopaenia;
 KW myelodysplastic syndrome; gene therapy refractory anaemia; aplastic anaemia; Fanconi's anaemia;
 KW chronic myelomonocytic leukaemia; aplastic anaemia; Fanconi's anaemia;
 KW pancythaemia; antibody; bone marrow transplant; cytoreductive therapy;
 KW cell expansion; stem cell mobilisation.
 XX OS Homo sapiens.
 XX PN US2002160004-A1.
 XX PD 31-OCT-2002.
 XX PF 13-MAR-2002; 2002US-00095449.
 XX PR 24-MAY-1993; 93US-00068394.
 PR 12-AUG-1993; 93US-00106463.
 PR 25-AUG-1993; 93US-00111758.
 PR 03-DEC-1993; 93US-00162407.
 PR 07-MAR-1994; 94US-00209502.
 PR 11-MAY-1994; 94US-00243545.
 PR 19-MAY-1995; 95US-00444632.
 PR 24-JUN-1996; 96US-00669632.
 XX (LYMAN/) LYMAN S D.
 PA (BECK/) BECKMANN M P.
 XX LYMAN SD, Beckmann MP;
 XX WPI: 2003-209211/20.
 DR N-PSDB; AX16545.
 XX New antibody binding mouse flt-3 ligand, useful for screening, diagnostic
 PT and biological assays in disorders with elevated serum levels of flt-3
 PT ligand, such as Fanconi's and myelodysplastic syndrome, aplastic and
 PT refractory anaemia.
 XX Example 4; Page 15-16; 18pp; English.
 XX The invention relates to an antibody that binds to mouse flt-3 ligand
 CC (flt-3 L) encoded by the cDNA insert in vector sfHAV-EO410 in Escherichia
 CC coli DH10B cells having American Type Culture Collection (ATCC) Accession
 CC No. 69286, where the ligand comprises the truncated extracellular domain
 CC of mouse flt-3 L. The methods and compositions are useful for screening,
 CC diagnostic and biological assays in disorders having elevated serum
 CC levels of flt-3 ligand, such as cancer, cytopaenia, myelodysplastic
 CC syndromes, stem cell disorders, refractory anaemia, chronic
 CC myelomonocytic leukaemia, aplastic anaemia, Fanconi's anaemia and
 CC pancythaemia. Flt3-L is also useful in allogeneic, syngeneic or
 CC autologous bone marrow transplants in patients undergoing cytoreductive
 CC therapies, as well as cell expansion. Flt3-L is also useful in gene
 CC therapy and progenitor and stem cell mobilisation systems. The present
 CC sequence represents human flt-3 L
 XX Sequence 235 AA;
 SQ Query Match 100.0%; Score 1242; DB 6; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAWSPPTTYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTY 60
 DB 1 MTVLAPAWSPPTTYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTY 60
 QY 61 ASNLQDEELCGGLWRLVLAQRWNERLKTIVAGSKQGLLERVNTTEIHFTVKCAFPQPPSCL 120
 DB 61 ASNLQDEELCGGLWRLVLAQRWNERLKTIVAGSKQGLLERVNTTEIHFTVKCAFPQPPSCL 120

QY 121 REVQTNISRLIQETSEQLVALKPWITRQNFRCLELQCCQDSSTLPPWSPRPLEATAPT 180
 DB 121 REVQTNISRLIQETSEQLVALKPWITRQNFRCLELQCCQDSSTLPPWSPRPLEATAPT 180
 QY 181 APQPPELLLLLPVGLLLLAACWCLHWQTRTRTPRGPGEQVPPVPSODLLIVH 235
 DB 181 APQPPELLLLLPVGLLLLAACWCLHWQTRTRTPRGPGEQVPPVPSODLLIVH 235
 RESULT 10
 ADD22874
 ID ADD22874 standard; protein; 235 AA.
 XX AC ADD22874;
 XX DT 15-JAN-2004 (first entry)
 XX DE Human flt3-ligand.
 XX KW flt-3 ligand; Fanconi's anaemia; acquired aplastic anaemia;
 KW myelodysplastic syndrome; human.
 XX OS Homo sapiens.
 XX PN US6630143-B1.
 XX PD 07-OCT-2003.
 XX PF 24-JUN-1996; 96US-00669692.
 XX PR 24-MAY-1993; 93US-00068394.
 PR 12-AUG-1993; 93US-00106463.
 PR 25-AUG-1993; 93US-00111758.
 PR 03-DEC-1993; 93US-00162407.
 PR 07-MAR-1994; 94US-00209502.
 PR 11-MAY-1994; 94US-00243545.
 PR 19-MAY-1995; 95US-00444632.
 XX (TMV) IMMUNEX CORP.
 PA LYMAN SD, Beckmann PM;
 PI WPI: 2003-810548/76.
 DR N-PSDB; ADD22873.
 XX New antibodies specifically binding to human flt-3 ligand, useful in
 PT immunoassays for measuring concentration of flt3-L in plasma or serum, or
 PT for predicting the status of a disease such as Fanconi's anemia or
 PT acquired aplastic anemia.
 XX Claim 5; SEQ ID NO 6; 17pp; English.
 XX The invention relates to an antibody that binds specifically to human flt
 CC -3 ligand. The antibodies that are immunoreactive with flt-3 ligand are
 CC useful in ELISA to measure concentration of flt3-L in plasma or serum,
 CC and predicting the status of a disease such as Fanconi's anaemia,
 CC acquired aplastic anaemia, or myelodysplastic syndromes. The present
 CC sequence represents the amino acid sequence of the human flt3-ligand.
 XX Sequence 235 AA;
 SQ Query Match 100.0%; Score 1242; DB 7; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAWSPPTTYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTY 60
 DB 1 MTVLAPAWSPPTTYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTY 60
 QY 61 ASNLQDEELCGGLWRLVLAQRWNERLKTIVAGSKQGLLERVNTTEIHFTVKCAFPQPPSCL 120
 DB 61 ASNLQDEELCGGLWRLVLAQRWNERLKTIVAGSKQGLLERVNTTEIHFTVKCAFPQPPSCL 120

QY 121 RFVQTNISRLLOETSEQLVAKPWITRQNFSCLELQCCPDSSSTLPPWSPRPLEATAPT 180
 DB 121 RFVQTNISRLLOETSEQLVAKPWITRQNFSCLELQCCPDSSSTLPPWSPRPLEATAPT 180
 QY 181 APQPPLLLLLPVGILLAAACWLMQRTTRTPRPGQVPPVSPQDLLLLVEH 235
 DB 181 APQPPLLLLLPVGILLAAACWLMQRTTRTPRPGQVPPVSPQDLLLLVEH 235

RESULT 11
 ADD80915
 ID ADD80915 standard; protein; 235 AA.
 XX AC ADD80915;
 XX DT 29-JAN-2004 (first entry)
 XX DE Amino acid sequence for human flt3-ligand.
 XX KW Cancer; dendritic cell; tumour-specific immune response; tumour growth;
 XX KW tumour incidence; tumour rejection; Flt3-ligand;
 XX KW haematopoietic progenitor; stem cell; immune response; cytostatic; human.
 XX OS Homo sapiens.
 XX PN US2003113341-A1.
 XX PD 19-JUN-2003.
 XX PF 11-SEP-2002; 2002US-00241927.
 XX PR 04-OCT-1995; 95US-00539142.
 XX PR 03-OCT-1996; 96US-00725540.
 XX PR 17-SEP-1998; 98US-00154903.
 XX PR 19-NOV-1999; 99US-00444027.
 XX PA (IMMV) IMMUNEX CORP.
 XX PI Lynch DH, Borges L, Miller RE, Maliszewski CR;
 XX WPI; 2003-851607/79.
 XX DR N-PSDB; ADD80914.
 XX PT Treating cancer, increasing the number of dendritic cells, augmenting
 PT tumour-specific immune response, and increasing tumor rejection in a
 PT patient having cancer by administering a composition comprising Flt3-
 PT ligand.
 XX PS Claim 12; SEQ ID NO 2; 15pp; English.
 XX CC The present invention relates to methods for treating cancer, increasing
 CC the number of dendritic cells, augmenting a tumour-specific immune
 CC response, reducing tumour growth, reducing tumour incidence, and
 CC increasing tumour rejection in a patient having cancer. The method
 CC involves administering a composition comprising Flt3-ligand. Flt3-ligand
 CC can generate large numbers of dendritic cells from haematopoietic
 CC progenitor and stem cells. Flt3-ligand can be used to augment an immune
 CC response in vivo. The methods of the invention are useful for treating
 CC cancer. The present sequence represents human flt3-ligand.
 XX SQ Sequence 235 AA;
 Query Match 100.0%; Score 1242; DB 7; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 DB 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

61 ASNLQDELCGGLWRLVLAQRWMLKTVAGSKMQGLLRRVNTIHFVTKCAFQPPPSCL 120

DB 61 ASNLQDELCGGLWRLVLAQRWMLKTVAGSKMQGLLRRVNTIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLLOETSEQLVAKPWITRQNFSCLELQCCPDSSSTLPPWSPRPLEATAPT 180
 DB 121 RFVQTNISRLLOETSEQLVAKPWITRQNFSCLELQCCPDSSSTLPPWSPRPLEATAPT 180
 QY 181 APQPPLLLLLPVGILLAAACWLMQRTTRTPRPGQVPPVSPQDLLLLVEH 235
 DB 181 APQPPLLLLLPVGILLAAACWLMQRTTRTPRPGQVPPVSPQDLLLLVEH 235

RESULT 12
 ADE48117
 ID ADE48117 standard; protein; 235 AA.
 XX AC ADE48117;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human Flt3-ligand.
 XX KW Flt3-ligand; vaccine; cancer; infection; human
 XX OS Homo sapiens.
 XX PN WO200303083-A2.
 XX PD 09-OCT-2003.
 XX PF 26-MAR-2003; 2003WO-US009773.
 XX PR 26-MAR-2002; 2002US-0368263P.
 XX PR 19-NOV-2002; 2002US-0427835P.
 XX PA (IMMV) IMMUNEX CORP.
 XX PI McKenna HJ, Liebowitz DN, Maliszewski CR;
 XX DR WPI; 2003-833534/77.
 XX PT Immunization protocols to enhance immune responses against vaccine
 PT antigens using an Flt3-ligand, useful for preventing or treating viral or
 PT bacterial infections, cancer, allergies, and fungal, parasitic and
 PT protozoal infections.
 XX PS Disclosure; SEQ ID NO 1; 96pp; English.
 XX CC The present invention relates to immunizing a subject by administering
 CC Flt3-ligand to a subject, optionally administering an auxiliary molecule,
 CC and administering a vaccine to the subject, where the vaccine comprises
 CC an antigen and an adjuvant. The methods and compositions of the present
 CC invention are useful for preventing and/or treating viral or bacterial
 CC infections, cancer, allergies, and fungal, parasitic, rickettsial and
 CC protozoal infections. The present sequence represents human Flt3-ligand.
 XX SQ Sequence 235 AA;
 Query Match 100.0%; Score 1242; DB 7; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 DB 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60

61 ASNLQDELCGGLWRLVLAQRWMLKTVAGSKMQGLLRRVNTIHFVTKCAFQPPPSCL 120

61 ASNLQDELCGGLWRLVLAQRWMLKTVAGSKMQGLLRRVNTIHFVTKCAFQPPPSCL 120

121 RFVQTNISRLLOETSEQLVAKPWITRQNFSCLELQCCPDSSSTLPPWSPRPLEATAPT 180

121 RFVQTNISRLLOETSEQLVAKPWITRQNFSCLELQCCPDSSSTLPPWSPRPLEATAPT 180

QY 181 APQPELLLLLLPVGLLLAAAWCLHWQTRRRTRPRGEGQVPPVPSQDLLLLVEH 235
 Db 181 APQPELLLLLLPVGLLLAAAWCLHWQTRRRTRPRGEGQVPPVPSQDLLLLVEH 235

RESULT 13

ID ADE80752 standard; protein; 235 AA.

XX AC ADE80752;

DT 29-JAN-2004 (first entry)

XX Microsatellite related FT3L wt ORF amino acid sequence.

XX frameshift mutation; microsatellite; cytostatic; neuroprotective;
 KW vasectropic; vaccine; gene therapy; neurodegenerative disorder;
 KW vascular disease; cancer.

XX Unidentified.

FN WO2003087162-A2.

PD 23-OCT-2003.

XX 17-APR-2003; 2003WO-EP004093.

XX 18-APR-2002; 2002EP-00008771.

PR 18-APR-2002; 2002EP-00008773.

PR 18-APR-2002; 2002EP-00008774.

XX (MTMM-) MTM LAB AG.

XX Von Knebel Doberitz M, Gebert J, Linnebacher M, Woerner S;

PI Riddler R, Bork P, Yuan YP;

XX WPI; 2003-845308/78.

XX New nucleic acid, useful in preparing a composition for diagnosing or

PS Claim 3; Fig 2; 62pp; English.

CC The present invention describes a nucleic acid sequence (I) which encodes
 CC a polypeptide consisting of TAF1B, MACS, JVRAG, EFVL3, TC6L1, ABCF1,
 CC AIMP2, CHD2, FL J11033, KIAA1032, ACVR2 or HU01 having a frameshift
 CC mutation. Also described: (1) a frameshift polypeptide (II); (2) a method
 CC for treating disorders associated with frameshift mutations in coding
 CC microsatellites; (3) a pharmaceutical composition comprising the nucleic
 CC acid and/or polypeptide; (4) a method for detecting a disorder associated
 CC with frameshift mutations in coding microsatellite regions; (5) a
 CC diagnostic or research kit for detecting a disorder associated with
 CC frameshift mutations in coding microsatellite regions, comprising the
 CC nucleic acid and/or frameshift polypeptide; and (6) a method for treating
 CC disorders associated with peptides arising from frameshift mutations in
 CC coding microsatellite regions in individuals. (I) and (II) have
 CC cytostatic, neuroprotective and vasotropic activities, and can be used in
 CC vaccines and in gene therapy. The nucleic acid (I) or frameshift
 CC polypeptide (II) can be used in detecting disorders associated with
 CC frameshift mutations in coding microsatellite regions or in preparing
 CC pharmaceutical compositions for treating disorders associated with
 CC frameshift mutations in coding microsatellite regions, e.g.,
 CC neurodegenerative disorder, vascular disease, cancer or precursory stages
 CC of cancer. The present sequence represents a protein used in the
 CC exemplification of the present invention.

XX Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 7; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.8e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
 Db 1 MTVLAPAWSPTTYLLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
 QY 61 ASNLQDEELCGGLMFLVLAQRMWELKTVAGSKWGLLERVNTTEHFVTKCAFQPPPSCL 120
 Db 61 ASNLQDEELCGGLMFLVLAQRMWELKTVAGSKWGLLERVNTTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQLQETSEQLVALKPWITRONFSCLELQCPDSSSTLPPWSPRPLEATAPT 180
 Db 121 RFVQTNISRLQLQETSEQLVALKPWITRONFSCLELQCPDSSSTLPPWSPRPLEATAPT 180
 QY 181 APQPELLLLLLPVGLLLAAAWCLHWQTRRRTRPRGEGQVPPVPSQDLLLLVEH 235
 Db 181 APQPELLLLLLPVGLLLAAAWCLHWQTRRRTRPRGEGQVPPVPSQDLLLLVEH 235

RESULT 14

AAG79950

ID AAG79950 standard; protein; 235 AA.

XX AC AAG79950;

DT 23-OCT-2003 (revised)

DT 16-MAY-2003 (first entry)

XX Secreted human protein comparison protein #2.

XX Gene; secreted; tyrosine kinase receptor ligand, subfamily;
 KW phosphorylation; kidney; blood; lung; brain glioblastoma; prostate;
 KW colon; leukocyte.

XX Unidentified.

XX WO2003002138-A1.

XX 09-JAN-2003.

XX 25-JUN-2002; 2002WO-US020172.

XX 27-JUN-2001; 2001US-00891498.

XX (PEKE) PE CORP NY.

XX Gong F, Ceccardi T, Ladunga I;

XX WPI; 2003-267895/26.

XX New isolated human secreted peptide and nucleic acids, useful for the
 PT development of human therapeutics and diagnostic compositions, drug
 PT screening assays, tissue typing and pharmacogenomic analysis.

XX Disclosure; Fig 2B; 66pp; English.

CC The sequences given in AAG79949-50 are included in the scope of the
 CC invention as they show high levels of similarity to the secreted peptide
 CC of the invention. The secreted protein is related to the tyrosine kinase
 CC receptor ligand subfamily. This protein effects protein phosphorylation.
 CC The human secreted peptides are useful in substantial and specific assays
 CC related to functional information of the peptide sequences, to raise
 CC antibodies or to elicit immune response, as reagents in assays that
 CC determine the levels of protein in biological fluids, and as markers for
 CC tissues where the corresponding protein is expressed. The peptides and
 CC the antibodies are useful in drug screening assays, tissue typing and
 CC pharmacogenomic analysis. The nucleic acid molecules are useful as
 CC probes, primers and chemical intermediates in biological assays, for
 CC constructing recombinant vectors, and expressing antigenic portions of
 CC the protein. The peptide and nucleic acid molecules are useful in the
 CC identification of therapeutic proteins and may serve as models or targets
 CC for the development of human therapeutic agents that modulate human
 CC secreted peptide activity in cells and tissues that express the secreted
 CC peptide, such as in kidney, blood, lung, brain glioblastoma, prostate,

CC colon or leukocytes. (Updated on 23-OCT-2003 to standardise OS field)

XX Sequence 235 AA;

Query Match 99.6%; Score 1237; DB 6; Length 235;

Best Local Similarity 99.6%; Pred. No. 1.7e-108;

Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

DB 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEIHFTVKCAFQPPPSCL 120

DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEIHFTVKCAFQPPPSCL 120

QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSTLPPWSPRPLEATAPT 180

DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSTLPPWSPRPLEATAPT 180

QY 181 APOPLLLLLLPGVGLLLAAACWCLHWQTRRTTRPRGQVPPVPSQDLLLLVEH 235

DB 181 APOPLLLLLLPGVGLLLAAACWCLHWQTRRTTRPRGQVPPVPSQDLLLLVEH 235

RESULT 15

AAR66175

ID AAR66175 standard; peptide; 235 AA.

AC AAR66175;

XX

DT 25-MAR-2003 (revised)

DT 10-AUG-1995 (first entry)

XX

XX Human S86/S109 Flt3 ligand peptide sequence.

DE

XX Flt3 ligand; tyrosine kinase receptor ligand.

KW

XX Homo sapiens.

OS

XX WO9426891-A2.

PN

XX

PD 24-NOV-1994.

PF

XX 18-MAY-1994; 94WO-US005150.

PR 19-MAY-1993; 93US-00065231.

PR 07-JUL-1993; 93US-00089283.

PR 16-JUL-1993; 93US-00092549.

PR 13-AUG-1993; 93US-00106340.

PR 24-AUG-1993; 93US-00112391.

PR 19-NOV-1993; 93US-00151111.

PR 03-DEC-1993; 93US-00162413.

XX

PA (SCHE) SCHERING CORP.

PA (INRM) INST NAT SANTE & RECH MEDICALE.

XX

XX Hannum CH, Lee FD, Birnbaum D, Culpepper JA;

XX

XX WPI; 1995-006787/01.

DR N-PSDB; AAQ79642.

XX

XX New ligand for the Flt3 tyrosine kinase receptor - and related nucleic acid, vectors, host cells and antibodies, useful for treating abnormal cell physiology and proliferation, e.g. cancer, also for diagnosis and drug screening.

PT

PT

PT

XX

XX Claim 11; Page 76-77; 90pp; English.

PS

XX

XX A cDNA library from the human stromal cell line 29SV48, in pME18S, was screened with an 800 bp fragment derived from mouse clone T118. This fragment encompasses the coding region conserved between two mouse clones, T118 and T110. Approx. 20 positive clones were selected and

CC partially sequenced. Two clones, S86 and S109, were found to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued to show homology to T110 until the stop codon, although to a lesser degree, for an overall homology of 66%. Clones T118 and S109 do not show homology to each other or to the other clones after mouse residue 163 (human residue 160). An additional mouse clone designated MB8 has a 29 AA insert at the junction between the common and divergent portions of the mouse ligand. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 235 AA;

Query Match 99.5%; Score 1236; DB 2; Length 235;

Best Local Similarity 99.6%; Pred. No. 2.1e-108;

Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

DB 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEIHFTVKCAFQPPPSCL 120

DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEIHFTVKCAFQPPPSCL 120

QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSTLPPWSPRPLEATAPT 180

DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSTLPPWSPRPLEATAPT 180

QY 181 APOPLLLLLLPGVGLLLAAACWCLHWQTRRTTRPRGQVPPVPSQDLLLLVEH 235

DB 181 APOPLLLLLLPGVGLLLAAACWCLHWQTRRTTRPRGQVPPVPSQDLLLLVEH 235

Search completed: April 8, 2004, 17:05:48

Job time : 66.4973 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 17:07:57 ; Search time 47.2554 Seconds
(without alignments)
1307.593 Million cell updates/sec

Title: US-08-994-468-6
Perfect score: 1242
Sequence: 1 MTVLAPAMSPPTVYLLILLLL.....RPGQVPPSPQDILLVH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	8	US-08-994-468-6
2	1242	100.0	235	9	US-09-904-536-1
3	1242	100.0	235	9	US-09-904-536-1
4	1242	100.0	235	9	US-09-904-536-1
5	1242	100.0	235	12	US-10-643-384-2
6	1242	100.0	235	13	US-10-095-449-6
7	1242	100.0	235	14	US-10-241-927-2
8	1242	100.0	235	14	US-10-314-035-6
9	1242	100.0	235	16	US-10-401-364-1
10	1236	99.5	235	15	US-10-116-273-174
11	1236	99.5	235	15	US-10-440-464-60
12	1124	90.5	212	9	US-09-904-536-10
13	1114	89.7	209	9	US-09-904-536-18
14	1110	89.4	209	9	US-09-904-536-9
15	1110	89.4	209	9	US-09-904-536-12

16	1110	89.4	209	9	US-09-904-536-14	Sequence 14, Appl
17	1110	89.4	209	9	US-09-904-536-17	Sequence 17, Appl
18	1108	89.2	209	9	US-09-904-536-11	Sequence 11, Appl
19	1108	89.2	209	9	US-09-904-536-15	Sequence 15, Appl
20	1107	89.1	209	9	US-09-904-536-13	Sequence 13, Appl
21	1106	89.0	209	9	US-09-904-536-8	Sequence 8, Appl
22	1100	88.6	209	9	US-09-904-536-16	Sequence 16, Appl
23	895.5	72.1	294	14	US-10-218-654-7	Sequence 7, Appl
24	895.5	72.1	294	14	US-10-262-439-7	Sequence 7, Appl
25	894.5	72.0	291	14	US-10-218-654-44	Sequence 44, Appl
26	894.5	72.0	291	14	US-10-262-439-44	Sequence 44, Appl
27	822	66.2	155	14	US-10-053-355A-1	Sequence 1, Appl
28	797.5	64.2	268	14	US-10-218-654-23	Sequence 23, Appl
29	797.5	64.1	276	14	US-10-262-439-23	Sequence 23, Appl
30	796.5	64.1	276	14	US-10-218-654-26	Sequence 26, Appl
31	796.5	64.1	276	14	US-10-262-439-26	Sequence 26, Appl
32	791.5	63.7	265	14	US-10-218-654-49	Sequence 49, Appl
33	791.5	63.7	265	14	US-10-262-439-49	Sequence 49, Appl
34	768.5	61.9	231	8	US-08-994-468-2	Sequence 2, Appl
35	768.5	61.9	231	9	US-09-448-378-2	Sequence 2, Appl
36	768.5	61.9	231	9	US-09-983-806-2	Sequence 2, Appl
37	768.5	61.9	231	13	US-10-095-449-2	Sequence 2, Appl
38	768.5	61.9	231	14	US-10-314-035-2	Sequence 2, Appl
39	768.5	61.9	231	16	US-10-401-364-2	Sequence 31, Appl
40	698.5	56.2	250	14	US-10-218-654-31	Sequence 31, Appl
41	698.5	56.2	250	14	US-10-262-439-31	Sequence 31, Appl
42	506.5	40.8	137	9	US-09-984-536-19	Sequence 19, Appl
43	97.5	7.9	558	14	US-10-304-946-14	Sequence 14, Appl
44	95.5	7.7	504	15	US-10-161-493-68	Sequence 68, Appl
45	95.5	7.7	517	14	US-10-271-078-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-994-468-6
; Sequence 6, Application US/08994468
; Publication No. US20030148516A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,468
; FILING DATE: 19-Dec-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,407
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-994-468-6
Query Match 100.0%; Score 1242; DB 8; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAPAWSPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
DB 1 MTVLAPAWSPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRYNTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRYNTEIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLQLCQPDSSSTLPPWSPRPLEATPT 180
DB 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLQLCQPDSSSTLPPWSPRPLEATPT 180
QY 181 APQPPILLLLLPVGLLLAAACLHWQTRTRTPRPGEQVPPVPSQDILLVEH 235
DB 181 APQPPILLLLLPVGLLLAAACLHWQTRTRTPRPGEQVPPVPSQDILLVEH 235
RESULT 2
US-09-448-378-1
Sequence 1, Application US/09448378
Patent No. US20020034517A1
GENERAL INFORMATION:
APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
FILE REFERENCE: 2836-D
CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent in version 3.0
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-448-378-1

Query Match 100.0%; Score 1242; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAPAWSPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
DB 1 MTVLAPAWSPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRYNTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRYNTEIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLQLCQPDSSSTLPPWSPRPLEATPT 180
DB 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLQLCQPDSSSTLPPWSPRPLEATPT 180
QY 181 APQPPILLLLLPVGLLLAAACLHWQTRTRTPRPGEQVPPVPSQDILLVEH 235
DB 181 APQPPILLLLLPVGLLLAAACLHWQTRTRTPRPGEQVPPVPSQDILLVEH 235

RESULT 3
US-09-983-806-6
Sequence 6, Application US/09983806
Patent No. US20020107365A1
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA: US/09/983,806
FILING DATE: 25-Oct-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-May-1995
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-983-806-6
Query Match 100.0%; Score 1242; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAPAWSPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
DB 1 MTVLAPAWSPTTYLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRYNTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRYNTEIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLQLCQPDSSSTLPPWSPRPLEATPT 180
DB 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLQLCQPDSSSTLPPWSPRPLEATPT 180
QY 181 APQPPILLLLLPVGLLLAAACLHWQTRTRTPRPGEQVPPVPSQDILLVEH 235
DB 181 APQPPILLLLLPVGLLLAAACLHWQTRTRTPRPGEQVPPVPSQDILLVEH 235

RESULT 4

US-09-904-536-1
 ; Sequence 1, Application US/09904536
 ; Patent No. US20020111475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/904.536
 ; CURRENT FILING DATE: 2001-07-16
 ; PRIOR APPLICATION NUMBER: 09/109,100
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-904-536-1

Query Match 100.0%; Score 1242; DB 9; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.1e-102;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 Db 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 QY 61 ASNLQDEELCGGLWRLVLAQRWNERLKTAVGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
 Db 61 ASNLQDEELCGGLWRLVLAQRWNERLKTAVGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLQLCCQPDSTLPPWSPRPLEATAPT 180
 Db 121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLQLCCQPDSTLPPWSPRPLEATAPT 180
 QY 181 APOPLLILLLLPVGLLLAAAWCLHWQTRRTTRPRGQVPPVPSQDLLLVEH 235
 Db 181 APOPLLILLLLPVGLLLAAAWCLHWQTRRTTRPRGQVPPVPSQDLLLVEH 235

RESULT 5

US-10-643-384-2
 ; Sequence 2, Application US/10643384
 ; Publication No. US20040037845A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brasel, Kenneth A.
 ; APPLICANT: Lyman, Stewart D.
 ; APPLICANT: Maraskovsky, Eugene
 ; APPLICANT: McKenna, Hilary J.
 ; APPLICANT: Lynch, David H.
 ; TITLE OF INVENTION: THE USE OF FLT3-LIGAND IN THE TREATMENT OF INFECTION
 ; FILE REFERENCE: 2836-H
 ; CURRENT APPLICATION NUMBER: US/10/643.384
 ; CURRENT FILING DATE: 2003-08-19
 ; PRIOR APPLICATION NUMBER: 10/241,927
 ; PRIOR FILING DATE: 2002-09-11
 ; PRIOR APPLICATION NUMBER: 09/444,027
 ; PRIOR FILING DATE: 1999-11-19
 ; PRIOR APPLICATION NUMBER: 09/154,903
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 08/725,540
 ; PRIOR FILING DATE: 1996-10-03
 ; PRIOR APPLICATION NUMBER: 08/539,142
 ; PRIOR FILING DATE: 1995-10-04
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Homo sapien

US-10-643-384-2

Query Match 100.0%; Score 1242; DB 12; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.1e-102;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 Db 1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 QY 61 ASNLQDEELCGGLWRLVLAQRWNERLKTAVGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
 Db 61 ASNLQDEELCGGLWRLVLAQRWNERLKTAVGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLQLCCQPDSTLPPWSPRPLEATAPT 180
 Db 121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLQLCCQPDSTLPPWSPRPLEATAPT 180
 QY 181 APOPLLILLLLPVGLLLAAAWCLHWQTRRTTRPRGQVPPVPSQDLLLVEH 235
 Db 181 APOPLLILLLLPVGLLLAAAWCLHWQTRRTTRPRGQVPPVPSQDLLLVEH 235

RESULT 6

US-10-095-449-6
 ; Sequence 6, Application US/10095449
 ; Publication No. US20020160004A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyman, Stewart D.
 ; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.0.1
 ; SOFTWARE: Microsoft Word, Version #5.1
 ; CURRENT APPLICATION NUMBER: US/10/095,449
 ; FILING DATE: 13-Mar-2002
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/669,692
 ; FILING DATE: 24-JUN-1996
 ; APPLICATION NUMBER: US/08/162,407
 ; FILING DATE: December 3, 1993
 ; APPLICATION NUMBER: 08/111,758
 ; FILING DATE: August 25, 1993
 ; APPLICATION NUMBER: 08/106,463
 ; FILING DATE: August 12, 1993
 ; APPLICATION NUMBER: 08/068,394
 ; FILING DATE: May 24, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Malaska, Stephen L.
 ; REGISTRATION NUMBER: 32,655
 ; REFERENCE/DOCKET NUMBER: 2813-C
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 235 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

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; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-095-449-6
Query Match 100.0%; Score 1242; DB 13; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
DB 1 MTVLAPAWSPTTYLLLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLERNVTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLERNVTEIHFVTKCAFQPPPSCL 120

QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLLELOCQDSDSTLPPWSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLLELOCQDSDSTLPPWSPRPLEATAPT 180

QY 181 APQPPLLLLLPVGLLLAAAWCLHWQTRRRTRPRGEGQVPPVPSQDLLLLVEH 235
DB 181 APQPPLLLLLPVGLLLAAAWCLHWQTRRRTRPRGEGQVPPVPSQDLLLLVEH 235

RESULT 7
US-10-241-927-2
; Sequence 2, Application US/10241927
; Publication No. US20030113341A1
; GENERAL INFORMATION:
; APPLICANT: Lynch, David H.
; APPLICANT: Borges, Luis
; APPLICANT: Miller, Robert E.
; APPLICANT: Maliszewski, Charles R.
; TITLE OF INVENTION: THE USE OF FLT3-LIGAND IN THE TREATMENT OF CANCER
; FILE REFERENCE: 2836-F
; CURRENT APPLICATION NUMBER: US/10/241,927
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 09/444,027
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/154,903
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/725,540
; PRIOR FILING DATE: 1996-10-03
; PRIOR APPLICATION NUMBER: US 08/539,142
; PRIOR FILING DATE: 1995-10-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-241-927-2

Query Match 100.0%; Score 1242; DB 14; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
DB 1 MTVLAPAWSPTTYLLLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLERNVTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLERNVTEIHFVTKCAFQPPPSCL 120

QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLLELOCQDSDSTLPPWSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLLELOCQDSDSTLPPWSPRPLEATAPT 180

QY 181 APQPPLLLLLPVGLLLAAAWCLHWQTRRRTRPRGEGQVPPVPSQDLLLLVEH 235
DB 181 APQPPLLLLLPVGLLLAAAWCLHWQTRRRTRPRGEGQVPPVPSQDLLLLVEH 235
```

```

RESULT 8
US-10-314-035-6
; Sequence 6, Application US/10314035
; Publication No. US20030157069A1
; GENERAL INFORMATION:
; APPLICANT: LYMAN, Stewart D.
; APPLICANT: BECKMANN, M. Patricia
; TITLE OF INVENTION: METHODS OF USING FLT3-LIGAND IN HEMATOPOIETIC CELL TRANSPLANTATI
; FILE REFERENCE: 2813-P
; CURRENT APPLICATION NUMBER: US/10/314,035
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US 08/994,468
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: US 08/444,627
; PRIOR FILING DATE: 1995-05-19
; PRIOR APPLICATION NUMBER: US 08/243,545
; PRIOR FILING DATE: 1994-05-11
; PRIOR APPLICATION NUMBER: US 08/209,502
; PRIOR FILING DATE: 1994-03-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-035-6

Query Match 100.0%; Score 1242; DB 14; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
DB 1 MTVLAPAWSPTTYLLLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60

QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLERNVTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLERNVTEIHFVTKCAFQPPPSCL 120

QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLLELOCQDSDSTLPPWSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLLELOCQDSDSTLPPWSPRPLEATAPT 180

QY 181 APQPPLLLLLPVGLLLAAAWCLHWQTRRRTRPRGEGQVPPVPSQDLLLLVEH 235
DB 181 APQPPLLLLLPVGLLLAAAWCLHWQTRRRTRPRGEGQVPPVPSQDLLLLVEH 235

RESULT 9
US-10-401-364-1
; Sequence 1, Application US/10401364
; Publication No. US20040022760A1
; GENERAL INFORMATION:
; APPLICANT: McKenna, Hilary J.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Maliszewski, Charles R.
; TITLE OF INVENTION: METHODS OF USING FLT3-LIGAND IN IMMUNIZATION PROTOCOLS
; FILE REFERENCE: 3399-B
; CURRENT APPLICATION NUMBER: US/10/401,364
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US 60/368,263
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/427,835
; PRIOR FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-364-1
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Query Match 100.0%; Score 1242; DB 16; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.1e-102;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 DB 1 MTVLAPAWSPTTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 QY 61 ASNLQDEELCGGLWRLVLAQRMWELKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
 DB 61 ASNLQDEELCGGLWRLVLAQRMWELKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLQCPDSSSTLPPPPSPRPLEATPT 180
 DB 121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLQCPDSSSTLPPPPSPRPLEATPT 180
 QY 181 APQPPELLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDILLVEH 235
 DB 181 APQPPELLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDILLVEH 235

RESULT 10
 US-10-116-275-174
 ; Sequence 174, Application US/10116275
 ; Publication No. US20030211476A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elan Pharmaceutical Technology
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Brayden, David
 ; APPLICANT: Byrne, Daragh
 ; APPLICANT: Lambkin, Imelda
 ; APPLICANT: Higgins, Lisa
 ; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
 ; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
 ; FILE REFERENCE: E1067/20087
 ; CURRENT APPLICATION NUMBER: US/10/116, 275
 ; CURRENT FILING DATE: 2002-10-04
 ; NUMBER OF SEQ ID NOS: 349
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 174
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-116-275-174

Query Match 99.5%; Score 1236; DB 15; Length 235;
 Best Local Similarity 99.6%; Pred. No. 3.7e-102;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 DB 1 MTVLAPAWSPTTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 QY 61 ASNLQDEELCGGLWRLVLAQRMWELKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
 DB 61 ASNLQDEELCGGLWRLVLAQRMWELKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLQCPDSSSTLPPPPSPRPLEATPT 180
 DB 121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLQCPDSSSTLPPPPSPRPLEATPT 180
 QY 181 APQPPELLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDILLVEH 235
 DB 181 APQPPELLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDILLVEH 235

RESULT 11
 US-10-440-464-60
 ; Sequence 60, Application US/10440464
 ; Publication No. US20040018528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DEPRIMO, SAMUEL
 ; APPLICANT: O'FARRELL, ANNE-MARIE

APPLICANT: MORIMOTO, ALYSSA
 APPLICANT: SMOLICH, BEVERLY
 APPLICANT: MANNING, WILLIAM
 APPLICANT: WALTER, SARAH
 APPLICANT: CHERRINGTON, JULIE
 APPLICANT: SCHILLING, JIM
 TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
 TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
 FILE REFERENCE: 038602/1592
 CURRENT APPLICATION NUMBER: US/10/440,464
 CURRENT FILING DATE: 2003-05-19
 PRIOR APPLICATION NUMBER: 60/380,872
 PRIOR FILING DATE: 2002-05-17
 PRIOR APPLICATION NUMBER: 60/448,922
 PRIOR FILING DATE: 2003-02-24
 PRIOR APPLICATION NUMBER: 60/448,874
 PRIOR FILING DATE: 2003-02-24
 NUMBER OF SEQ ID NOS: 185
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 60
 LENGTH: 235
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-440-464-60

Query Match 99.5%; Score 1236; DB 15; Length 235;
 Best Local Similarity 99.6%; Pred. No. 3.7e-102;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 DB 1 MTVLAPAWSPTTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 QY 61 ASNLQDEELCGGLWRLVLAQRMWELKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
 DB 61 ASNLQDEELCGGLWRLVLAQRMWELKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLQCPDSSSTLPPPPSPRPLEATPT 180
 DB 121 RFVQTNISRLLOETSEQLVALKPWITRONFSRCLQCPDSSSTLPPPPSPRPLEATPT 180
 QY 181 APQPPELLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDILLVEH 235
 DB 181 APQPPELLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDILLVEH 235

RESULT 12
 US-09-904-536-10
 ; Sequence 10, Application US/09904536
 ; Patent No. US20020111475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/904,536
 ; CURRENT FILING DATE: 2001-07-16
 ; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-904-536-10

Query Match 90.5%; Score 1124; DB 9; Length 212;
 Best Local Similarity 100.0%; Pred. No. 3.2e-92;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTASNLQDEELCGGLWRLVLAQRMW 84

Db 2 SGTDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWME 61
 Qy 85 RLKTVAGSKMQLLERVNTIHFVTKCAFPQPPSCFLRFVQTNISRLLOETSEQLVAKPW 144
 Db 62 RLKTVAGSKMQLLERVNTIHFVTKCAFPQPPSCFLRFVQTNISRLLOETSEQLVAKPW 121
 Qy 145 ITRQNFRCLELQCCPDSSSTLPPWSPRPLEATAPQPPPLLLLLLPGVLLLAANWC 204
 Db 122 ITRQNFRCLELQCCPDSSSTLPPWSPRPLEATAPQPPPLLLLLLPGVLLLAANWC 181
 Qy 205 LHMORTRRTPRGEQVPPVPSQDLLLLVEH 235
 Db 182 LHMORTRRTPRGEQVPPVPSQDLLLLVEH 212

RESULT 13

US-09-904-536-18
 ; Sequence 18, Application US/09904536
 ; Patent No. US20020111475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/904,536
 ; CURRENT FILING DATE: 2001-07-16
 ; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-904-536-18

Query Match 89.7%; Score 1114; DB 9; Length 209;
 Best Local Similarity 100.0%; Pred. No. 2.4e-91; Indels 0; Gaps 0;
 Matches 209; Conservative 0; Mismatches 0;
 Qy 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWME 86
 Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWME 60
 Qy 87 KTVAGSKMQLLERVNTIHFVTKCAFPQPPSCFLRFVQTNISRLLOETSEQLVAKPWIT 146
 Db 61 KTVAGSKMQLLERVNTIHFVTKCAFPQPPSCFLRFVQTNISRLLOETSEQLVAKPWIT 120
 Qy 147 RQNFRCLELQCCPDSSSTLPPWSPRPLEATAPQPPPLLLLLLPGVLLLAANWC 206
 Db 121 RQNFRCLELQCCPDSSSTLPPWSPRPLEATAPQPPPLLLLLLPGVLLLAANWC 180
 Qy 207 WQTRRRTPRGEQVPPVPSQDLLLLVEH 235
 Db 181 WQTRRRTPRGEQVPPVPSQDLLLLVEH 209

RESULT 14

US-09-904-536-9
 ; Sequence 9, Application US/09904536
 ; Patent No. US20020111475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/904,536
 ; CURRENT FILING DATE: 2001-07-16
 ; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9

; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-904-536-9
 Query Match 89.4%; Score 1110; DB 9; Length 209;
 Best Local Similarity 99.5%; Pred. No. 5.5e-91;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWME 86
 Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWME 60
 Qy 87 KTVAGSKMQLLERVNTIHFVTKCAFPQPPSCFLRFVQTNISRLLOETSEQLVAKPWIT 146
 Db 61 KTVAGSKMQLLERVNTIHFVTKCAFPQPPSCFLRFVQTNISRLLOETSEQLVAKPWIT 120
 Qy 147 RQNFRCLELQCCPDSSSTLPPWSPRPLEATAPQPPPLLLLLLPGVLLLAANWC 206
 Db 121 RQNFRCLELQCCPDSSSTLPPWSPRPLEATAPQPPPLLLLLLPGVLLLAANWC 180
 Qy 207 WQTRRRTPRGEQVPPVPSQDLLLLVEH 235
 Db 181 WQTRRRTPRGEQVPPVPSQDLLLLVEH 209

RESULT 15

US-09-904-536-12
 ; Sequence 12, Application US/09904536
 ; Patent No. US20020111475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/904,536
 ; CURRENT FILING DATE: 2001-07-16
 ; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-904-536-12

Query Match 89.4%; Score 1110; DB 9; Length 209;
 Best Local Similarity 99.5%; Pred. No. 5.5e-91;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWME 86
 Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWME 60
 Qy 87 KTVAGSKMQLLERVNTIHFVTKCAFPQPPSCFLRFVQTNISRLLOETSEQLVAKPWIT 146
 Db 61 KTVAGSKMQLLERVNTIHFVTKCAFPQPPSCFLRFVQTNISRLLOETSEQLVAKPWIT 120
 Qy 147 RQNFRCLELQCCPDSSSTLPPWSPRPLEATAPQPPPLLLLLLPGVLLLAANWC 206
 Db 121 RQNFRCLELQCCPDSSSTLPPWSPRPLEATAPQPPPLLLLLLPGVLLLAANWC 180
 Qy 207 WQTRRRTPRGEQVPPVPSQDLLLLVEH 235
 Db 181 WQTRRRTPRGEQVPPVPSQDLLLLVEH 209

Search completed: April 8, 2004, 17:17:20
 Job time : 48.2554 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 17:03:57 ; Search time 21.0734 Seconds

(without alignments)
575.708 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242

Sequence: 1 MVLAPAWSPPTVYLLILL.....RPGQVPPVSPQDLLVH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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3: /cgn2_6/prodata/2/iaa/6A-COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1	US-08-243-545-6
2	1242	100.0	235	2	US-08-993-962-6
3	1242	100.0	235	3	US-09-160-841-6
4	1242	100.0	235	3	US-09-109-100-1
5	1242	100.0	235	4	US-08-669-692-6
6	1242	100.0	235	4	US-08-444-626-6
7	1242	100.0	235	5	PCT-US94-05365-6
8	1124	90.5	212	3	US-09-109-100-10
9	1114	89.7	209	3	US-09-109-100-18
10	1110	89.4	209	3	US-09-109-100-9
11	1110	89.4	209	3	US-09-109-100-12
12	1110	89.4	209	3	US-09-109-100-14
13	1110	89.4	209	3	US-09-109-100-17
14	1108	89.2	209	3	US-09-109-100-11
15	1108	89.2	209	3	US-09-109-100-15
16	1107	89.1	209	3	US-09-109-100-13
17	1106	89.0	209	3	US-09-109-100-8
18	1100	88.6	209	3	US-09-109-100-16
19	895.5	72.1	294	4	US-09-322-409-7
20	895.5	72.1	294	4	US-09-451-527-7
21	894.5	72.0	291	4	US-09-322-409-44
22	894.5	72.0	291	4	US-09-451-527-44
23	797.5	64.2	268	4	US-09-322-409-23
24	797.5	64.2	268	4	US-09-451-527-23
25	796.5	64.1	275	4	US-09-322-409-26
26	796.5	64.1	275	4	US-09-451-527-26
27	791.5	63.7	265	4	US-09-322-409-49

28 791.5 63.7 265 4 US-09-451-527-49
29 768.5 61.9 231 1 US-08-243-545-2
30 768.5 61.9 231 2 US-08-993-962-2
31 768.5 61.9 231 3 US-09-160-841-2
32 768.5 61.9 231 4 US-08-669-692-2
33 768.5 61.9 231 4 US-08-444-626-2
34 768.5 61.9 231 5 PCT-US94-05365-2
35 765.5 61.6 231 1 US-08-220-379B-7
36 765.5 61.6 231 5 PCT-US95-03866-6
37 698.5 56.2 250 4 US-09-322-409-31
38 698.5 56.2 250 4 US-09-451-527-31
39 506.5 40.8 137 3 US-09-109-100-19
40 154 12.4 42 5 PCT-US94-05150-17
41 91.5 7.4 675 1 US-08-317-522A-9
42 91.5 7.4 675 1 US-08-439-818A-9
43 91.5 7.4 675 2 US-08-751-965-9
44 91.5 7.4 675 2 US-08-738-975-9
45 91.5 7.4 675 2 US-08-728-626-9

ALIGNMENTS

RESULT 1
US-08-243-545-6
; Sequence 6, Application US/08243545
; Patent No. 5554512
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,545
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: *756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids

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/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-243-545-6

Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.9e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPPTTYLLLLLLSSGLSGTQDCSPFHSPISSDFAVKIRELSYLLQDYPVTV 60
Db 1 MTVLAPAWSPPTTYLLLLLLSSGLSGTQDCSPFHSPISSDFAVKIRELSYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLLOETSEQLVAKPWITRONFSCLQLQCPDSSSTLPPWSPRPLEATPT 180
Db 121 RFVQTNISRLLOETSEQLVAKPWITRONFSCLQLQCPDSSSTLPPWSPRPLEATPT 180
QY 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDILLVH 235
Db 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDILLVH 235

RESULT 2
US-08-993-962-6
/ Sequence 6, Application US/08993962
/ Patent No. 5843423
/ GENERAL INFORMATION:
/ APPLICANT: Lyman, Stewart D.
/ APPLICANT: Beckmann, M. Patricia
/ TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Stephen L. Malaska, Immunex Corporation
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 7.0.1
/ SOFTWARE: Microsoft Word, Version #5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/993,962
/ FILING DATE: December 18, 1997
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/162,407
/ FILING DATE: December 3, 1993
/ APPLICATION NUMBER: 08/111,758
/ FILING DATE: August 25, 1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/106,463
/ FILING DATE: August 12, 1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/068,394
/ FILING DATE: May 24, 1993
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Malaska, Stephen L.
/ REGISTRATION NUMBER: 32,655
/ REFERENCE/DOCKET NUMBER: 2813-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 587-0430
/ TELEFAX: (206) 233-0644
/ TELEX: 756822

/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 235 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-993-962-6

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.9e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPPTTYLLLLLLSSGLSGTQDCSPFHSPISSDFAVKIRELSYLLQDYPVTV 60
Db 1 MTVLAPAWSPPTTYLLLLLLSSGLSGTQDCSPFHSPISSDFAVKIRELSYLLQDYPVTV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLERNVTEHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLLOETSEQLVAKPWITRONFSCLQLQCPDSSSTLPPWSPRPLEATPT 180
Db 121 RFVQTNISRLLOETSEQLVAKPWITRONFSCLQLQCPDSSSTLPPWSPRPLEATPT 180
QY 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDILLVH 235
Db 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDILLVH 235

RESULT 3
US-09-160-841-6
/ Sequence 6, Application US/09160841
/ Patent No. 6190655
/ GENERAL INFORMATION:
/ APPLICANT: Lyman, Stewart D.
/ APPLICANT: Beckmann, M. Patricia
/ TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Stephen L. Malaska, Immunex Corporation
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 7.0.1
/ SOFTWARE: Microsoft Word, Version #5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/160,841
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/162,407
/ FILING DATE: December 3, 1993
/ APPLICATION NUMBER: 08/111,758
/ FILING DATE: August 25, 1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/106,463
/ FILING DATE: August 12, 1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/068,394
/ FILING DATE: May 24, 1993
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Malaska, Stephen L.
/ REGISTRATION NUMBER: 32,655
/ REFERENCE/DOCKET NUMBER: 2813-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 587-0430
/ TELEFAX: (206) 233-0644
/ TELEX: 756822
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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 235 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-160-841-6

Query Match      100.0%; Score 1242; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.9e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLPAWSPPTVYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
DB 1 MTVLPAWSPPTVYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRRVNTIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRRVNTIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLLOETSQLVAKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATPT 180
DB 121 RFVQTNISRLLOETSQLVAKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATPT 180
QY 181 APQPPLLLLLLPVGLLLAAACLHWQTRRRTRPRGQVPPVPSQDLLLLVEH 235
DB 181 APQPPLLLLLLPVGLLLAAACLHWQTRRRTRPRGQVPPVPSQDLLLLVEH 235

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RESULT 4
US-09-109-100-1
; Sequence 1, Application US/09109100C
; Patent No. 6231661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-1

Query Match      100.0%; Score 1242; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.9e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLPAWSPPTVYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
DB 1 MTVLPAWSPPTVYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRRVNTIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRRVNTIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLLOETSQLVAKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATPT 180
DB 121 RFVQTNISRLLOETSQLVAKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATPT 180
QY 181 APQPPLLLLLLPVGLLLAAACLHWQTRRRTRPRGQVPPVPSQDLLLLVEH 235
DB 181 APQPPLLLLLLPVGLLLAAACLHWQTRRRTRPRGQVPPVPSQDLLLLVEH 235

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RESULT 5
US-08-669-692-6
; Sequence 6, Application US/08669692
; Patent No. 6630143

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; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,692
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 235 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-669-692-6

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Query Match      100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.9e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLPAWSPPTVYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
DB 1 MTVLPAWSPPTVYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRRVNTIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRRVNTIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLLOETSQLVAKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATPT 180
DB 121 RFVQTNISRLLOETSQLVAKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATPT 180
QY 181 APQPPLLLLLLPVGLLLAAACLHWQTRRRTRPRGQVPPVPSQDLLLLVEH 235
DB 181 APQPPLLLLLLPVGLLLAAACLHWQTRRRTRPRGQVPPVPSQDLLLLVEH 235

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RESULT 6
US-08-444-626-6
; Sequence 6, Application US/08444626

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Patent No. 6632424
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-626-6

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.9e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAPAWSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60
Db 1 MTVLAPAWSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
QY 121 RVQVQNISSLQETSEQLVAKPWITRQNFRCLELQCPDSSITLPPFPWSPRPLEATAPT 180
Db 121 RVQVQNISSLQETSEQLVAKPWITRQNFRCLELQCPDSSITLPPFPWSPRPLEATAPT 180
QY 181 APQPELLLLLLPVGLLLIAAWCLHWQTRRRTPRPGEQVPPVPSQDILLVHH 235
Db 181 APQPELLLLLLPVGLLLIAAWCLHWQTRRRTPRPGEQVPPVPSQDILLVHH 235

RESULT 7

PCT-US94-05365-6
Sequence 6, Application PC/TUS9405365
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05365-6

Query Match 100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.9e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVLAPAWSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60
Db 1 MTVLAPAWSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120

Db 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLVRVNTIHFVTKCAFQPPSPCL 120
QY 121 RFVQTNISRLLOETSEQLVAKPWITRQNFSCLELQCPDSSSTLPPWSPRPLEATPT 180
Db 121 RFVQTNISRLLOETSEQLVAKPWITRQNFSCLELQCPDSSSTLPPWSPRPLEATPT 180
QY 181 AQCPULLLLLPVGLLLAAWCLHWQTRTRPRGEGVPPVPSQDILLVEH 235
Db 181 AQCPULLLLLPVGLLLAAWCLHWQTRTRPRGEGVPPVPSQDILLVEH 235
RESULT 8
US-09-109-100-10
; Sequence 10, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-10
Query Match 90.5%; Score 1124; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.6e-105;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 SGTQCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWME 84
Db 2 SGTQCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWME 61
QY 85 RLKTVAGSKMOGLLVRVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPW 144
Db 62 RLKTVAGSKMOGLLVRVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPW 121
QY 145 ITRQNFSCLELQCPDSSSTLPPWSPRPLEATPTAQPPLLLLLLPVGLLLAAWCLH 204
Db 122 ITRQNFSCLELQCPDSSSTLPPWSPRPLEATPTAQPPLLLLLLPVGLLLAAWCLH 181
QY 205 LHWQTRTRPRGEGVPPVPSQDILLVEH 235
Db 182 LHWQTRTRPRGEGVPPVPSQDILLVEH 212
RESULT 9
US-09-109-100-10
; Sequence 18, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-10
Query Match 89.7%; Score 1114; DB 3; Length 209;
Best Local Similarity 100.0%; Pred. No. 2.6e-104;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWML 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWML 60
QY 87 KTVAGSKMOGLLVRVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 146
Db 61 KTVAGSKMOGLLVRVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 120
QY 147 RQNFSCLELQCPDSSSTLPPWSPRPLEATPTAQPPLLLLLLPVGLLLAAWCLH 206
Db 121 RQNFSCLELQCPDSSSTLPPWSPRPLEATPTAQPPLLLLLLPVGLLLAAWCLH 180
QY 207 WQTRRTTRPRGEGVPPVPSQDILLVEH 235
Db 181 WQTRRTTRPRGEGVPPVPSQDILLVEH 209

RESULT 10

US-09-109-100-9

; Sequence 9, Application US/09109100C

; Patent No. 6291661

; GENERAL INFORMATION:

; APPLICANT: Graddis, Thomas J.

; APPLICANT: McGrew, Jeffrey T.

; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE

; FILE REFERENCE: 03260.0028

; CURRENT APPLICATION NUMBER: US/09/109,100C

; CURRENT FILING DATE: 1998-07-02

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 9

; LENGTH: 209

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-109-100-9

Query Match 89.4%; Score 1110; DB 3; Length 209;

Best Local Similarity 99.5%; Pred. No. 6.5e-104;

Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWML 86

Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWML 60

QY 87 KTVAGSKMOGLLVRVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 146

Db 61 KTVAGSKMOGLLVRVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 120

QY 147 RQNFSCLELQCPDSSSTLPPWSPRPLEATPTAQPPLLLLLLPVGLLLAAWCLH 206

Db 121 RQNFSCLELQCPDSSSTLPPWSPRPLEATPTAQPPLLLLLLPVGLLLAAWCLH 180

QY 207 WQTRRTTRPRGEGVPPVPSQDILLVEH 235

Db 181 WQTRRTTRPRGEGVPPVPSQDILLVEH 209

RESULT 11

US-09-109-100-12

; Sequence 12, Application US/09109100C

; Patent No. 6291661

; GENERAL INFORMATION:

; APPLICANT: Graddis, Thomas J.

; APPLICANT: McGrew, Jeffrey T.

; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE

; FILE REFERENCE: 03260.0028

; CURRENT APPLICATION NUMBER: US/09/109,100C

; CURRENT FILING DATE: 1998-07-02

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 12

; LENGTH: 209

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-12

Query Match      89.4%; Score 1110; DB 3; Length 209;
Best Local Similarity 99.5%; Pred. No. 6.5e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLODEELCGGLWRLVLAQRWNERL 86
Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLODEELCGGLWRLVLAQRWNERL 60

QY 87 KTVAGSKMQGLLERVNTTEHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 146
Db 61 KTVAGSKMQGLLERVNTTEHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 120

QY 147 RQNFSCRLELCQPDSSSTLPPWSPRPLEATAPQPPPLLLLLLVGLLLAAWCLH 206
Db 121 RQNFSCRLELCQPDSSSTLPPWSPRPLEATAPQPPPLLLLLLVGLLLAAWCLH 180

QY 207 WQTRRTTRPRGQVPPVPSQDLLLLVEH 235
Db 181 WQTRRTTRPRGQVPPVPSQDLLLLVEH 209

RESULT 12
US-09-109-100-14
; Sequence 14, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-14

Query Match      89.4%; Score 1110; DB 3; Length 209;
Best Local Similarity 99.5%; Pred. No. 6.5e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLODEELCGGLWRLVLAQRWNERL 86
Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLODEELCGGLWRLVLAQRWNERL 60

QY 87 KTVAGSKMQGLLERVNTTEHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 146
Db 61 KTVAGSKMQGLLERVNTTEHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 120

QY 147 RQNFSCRLELCQPDSSSTLPPWSPRPLEATAPQPPPLLLLLLVGLLLAAWCLH 206
Db 121 RQNFSCRLELCQPDSSSTLPPWSPRPLEATAPQPPPLLLLLLVGLLLAAWCLH 180

QY 207 WQTRRTTRPRGQVPPVPSQDLLLLVEH 235
Db 181 WQTRRTTRPRGQVPPVPSQDLLLLVEH 209

RESULT 13
US-09-109-100-17
; Sequence 17, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-17

Query Match      89.4%; Score 1110; DB 3; Length 209;
Best Local Similarity 99.5%; Pred. No. 6.5e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLODEELCGGLWRLVLAQRWNERL 86
Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLODEELCGGLWRLVLAQRWNERL 60

QY 87 KTVAGSKMQGLLERVNTTEHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 146
Db 61 KTVAGSKMQGLLERVNTTEHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 120

QY 147 RQNFSCRLELCQPDSSSTLPPWSPRPLEATAPQPPPLLLLLLVGLLLAAWCLH 206
Db 121 RQNFSCRLELCQPDSSSTLPPWSPRPLEATAPQPPPLLLLLLVGLLLAAWCLH 180

QY 207 WQTRRTTRPRGQVPPVPSQDLLLLVEH 235
Db 181 WQTRRTTRPRGQVPPVPSQDLLLLVEH 209

RESULT 14
US-09-109-100-11
; Sequence 11, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-11

Query Match      89.2%; Score 1108; DB 3; Length 209;
Best Local Similarity 99.3%; Pred. No. 1e-103;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLODEELCGGLWRLVLAQRWNERL 86
Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLODEELCGGLWRLVLAQRWNERL 60

QY 87 KTVAGSKMQGLLERVNTTEHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 146
Db 61 KTVAGSKMQGLLERVNTTEHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVAKPWIT 120

QY 147 RQNFSCRLELCQPDSSSTLPPWSPRPLEATAPQPPPLLLLLLVGLLLAAWCLH 206
Db 121 RQNFSCRLELCQPDSSSTLPPWSPRPLEATAPQPPPLLLLLLVGLLLAAWCLH 180

QY 207 WQTRRTTRPRGQVPPVPSQDLLLLVEH 235
Db 181 WQTRRTTRPRGQVPPVPSQDLLLLVEH 209

RESULT 15
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US-09-109-100-15
; Sequence 15, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-15

Query Match 89.2%; Score 1108; DB 3; Length 209;
Best Local Similarity 99.5%; Pred. No. 1e-103;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWVERL 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWVERL 60
Qy 87 KTVAGSKKQGLLERVNTIEHFVTKCAFQPPSCILRFVQTNISRLLOETSEQLVAKPWIT 146
Db 61 KTVAGSKKQGLLERVNTIEHFVTKCAFQPPSCILRFVQTNISRLLOETSEQLVAKPWIT 120
Qy 147 RQNFSCLELOCOPDSSTLPPWSPRPLEATAPTAPQPPPLLLLLLFPVGLLLIAAAWCLH 206
Db 121 RQNFSCLELOCOPDSSTLPPWSPRPLEATAPTAPQPPPLLLLLLFPVGLLLIAAAWCLH 180
Qy 207 WQTRRRTPRGEQVPPVPSQDLLLLVEH 235
Db 181 WQTRRRTPRGEQVPPVPSQDLLLLVEH 209

Search completed: April 8, 2004, 17:09:11
Job time : 22.0734 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 17:03:02 ; Search time 10.1196 Seconds
(without alignments)
1264.231 Million cell updates/sec

Title: US-08-994-468-6_COPY_28_160

Perfect score: 701

Sequence: 1 QDCSFQSPISDFAVKIRE.....LKPWITQNSRCLELQCCP 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	701	100.0	178	I39076	Flt3 ligand altern
2	701	100.0	235	I38440	flt3 ligand - huma
3	695	99.1	245	S43293	FLT3/FLK2 ligand (
4	508	72.5	220	S43291	FLT3/FLK2 ligand (
5	508	72.5	220	I58343	flt3 ligand isoform
6	508	72.5	231	A49265	flt3/flk-2 ligand
7	78	11.1	205	S76666	hypothetical prote
8	77	11.0	872	E71852	valine-tRNA ligase
9	75.5	10.8	315	F97827	dimethyladenosine
10	75	10.7	297	F98615	hypothetical prote
11	74.5	10.6	388	S28798	hypothetical prote
12	74.5	10.6	1188	C71231	hypothetical prote
13	72.5	10.3	398	T52311	isopenicillin N ep
14	72	10.3	362	A37783	iodopsin - chicken
15	71.5	10.2	832	C72278	alpha-mannosidase
16	71	10.1	341	A82129	fatty acid/phospho
17	71	10.1	661	TNBE12	74k alpha trans-in
18	71	10.1	663	C70838	probable zinc meta
19	70.5	10.1	285	AG1535	transport protein
20	70.5	10.1	499	T49049	hypothetical prote
21	70.5	10.1	1858	A44214	genome polyprotein
22	70	10.0	150	E98044	ABC transporter, t
23	70	10.0	553	C83866	hypothetical prote
24	69.5	9.9	321	T08687	P52IRPK protein ho
25	69.5	9.9	474	T19543	hypothetical prote
26	69	9.8	414	A23242	hypothetical prote
27	69	9.8	874	A64664	valine-tRNA ligase
28	69	9.8	1011	A12046	ABC transporter AT
29	69	9.8	4324	T50176	Probable peptide s

30	68.5	9.8	363	S75088	probable GTP-bindin
31	68.5	9.8	885	B86257	NBS/LRR disease re
32	68	9.7	566	S29233	testis-specific pr
33	67.5	9.6	234	AF2224	hypothetical prote
34	67.5	9.6	396	A95038	glucuronyl hydrola
35	67.5	9.6	396	D97908	unsaturated glucur
36	67.5	9.6	497	RNFSN	transcription init
37	67.5	9.6	1308	B75198	DNA helicase relat
38	67	9.6	187	A45878	hypothetical prote
39	67	9.6	444	S31191	tubulin beta-1 cha
40	67	9.6	506	A45841	T-complex-associat
41	67	9.6	781	AC2086	hypothetical prote
42	67	9.6	1893	A56158	eye development pr
43	67	9.6	2126	H70621	probable polyketid
44	66.5	9.5	497	JQ0338	transcription init
45	66	9.4	364	OOHUR	opsin, red-sensiti

ALIGNMENTS

RESULT 1

I39076

Flt3 ligand alternatively spliced isoform - human

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C/Accession: I39076

R/Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.

Oncogene 11, 1165-1172, 1995

A/Title: Structural analysis of human and murine flt3 ligand genomic loci.

A/Reference number: I39075; MUID:96032581; PMID:7566977

A/Accession: I39076

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-178 <RES>

A/Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038

C/Genetics:

A/Introns: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match 100.0%; Score 701; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 9.8e-66;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/	1	QDCSFQSPISDFAVKIRELSDYLLQDPVTVASNLQDEELCGGLWRLVLAQRMWERLK 60
Db	28	QDCSFQSPISDFAVKIRELSDYLLQDPVTVASNLQDEELCGGLWRLVLAQRMWERLK 87
Q/	61	TVAGSKXQGLLERVNTTEIHFVTKCAFQPPSPCLRFVQTNISRLLOSTSEQLVALKPWITR 120
Db	88	TVAGSKXQGLLERVNTTEIHFVTKCAFQPPSPCLRFVQTNISRLLOSTSEQLVALKPWITR 147
Q/	121	QNSRCLELQCCP 133
Db	148	QNSRCLELQCCP 160

RESULT 2

I38440

flt3 ligand - human

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000

C/Accession: I38440; I39075; S43292

R/Lyman, S.D.; James, L.; Johnson, L.; Braseel, K.; de Vries, P.; Escobar, S.S.; Downey,

Blood 83, 2795-2801, 1994

A/Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor for e

A/Reference number: I38440; MUID:94235842; PMID:8180375

A/Accession: I38440

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-235 <RES>

A/Cross-references: EMBL:U03858; NID:g494978; PIDN:AAA19825.1; PID:g494979

R/Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.

Oncogene 11, 1165-1172, 1995

A;Title: Structural analysis of human and murine flt3 ligand genomic loci.
A;Reference number: I39075; MUID:96032581; PMID:7566977
A;Accession: I39075
A;Status: preliminary; translated from GB/EMBL/DDB3
A;Molecule type: DNA
A;Residues: 1-235 <RE2>
A;Cross-references: EMBL:U29874; NID:g1072036; PID:AAA90949.1; PID:g1072037
R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.
Nature 368, 643-648, 1994
A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic cells.
A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Accession: S43290
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-245 <HAN>
A;Cross-references: GB:U04806; NID:g483844; PID:AAA17999.1; PID:g483845
A;Note: the authors translated the codon AGT for residue 25 as Met.
C;Genetics:
A;Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3
Query Match 100.0%; Score 701; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QDCSFQHSPTSSDFAVKIRELSYLLQDYFVTVASNLQDEELCGGLRWLVLAQRWVERLK 60
DB 28 QDCSFQHSPTSSDFAVKIRELSYLLQDYFVTVASNLQDEELCGGLRWLVLAQRWVERLK 87
QY 61 TVAGSKMQLLERNVTEIHFTVKAFQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 120
DB 88 TVAGSKMQLLERNVTEIHFTVKAFQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 147
QY 121 QNFSRCLELOQCP 133
DB 148 QNFSRCLELOQCP 160
RESULT 3
S43293
FLT3/FLK2 ligand (clone S109) - human
C;Species: Homo sapiens (man)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.
Nature 368, 643-648, 1994
A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic cells.
A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Accession: S43293
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-245 <HAN>
A;Note: the authors translated the codon AGT for residue 25 as Met
Query Match 99.1%; Score 695; DB 2; Length 245;
Best Local Similarity 99.2%; Pred. No. 6.1e-65;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QDCSFQHSPTSSDFAVKIRELSYLLQDYFVTVASNLQDEELCGGLRWLVLAQRWVERLK 60
DB 28 QDCSFQHSPTSSDFAVKIRELSYLLQDYFVTVASNLQDEELCGGLRWLVLAQRWVERLK 87
QY 61 TVAGSKMQLLERNVTEIHFTVKAFQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 120
DB 88 TVAGSKMQLLERNVTEIHFTVKAFQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 147
QY 121 QNFSRCLELOQCP 133
DB 148 QNFSRCLELOQCP 160
RESULT 4
S43291
FLT3/FLK2 ligand (clone T118) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.
Nature 368, 643-648, 1994
A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic cells.
A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Accession: S43291
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-220 <HAN>
Query Match 72.5%; Score 508; DB 2; Length 220;
Best Local Similarity 73.9%; Pred. No. 1.8e-45;
Matches 99; Conservative 12; Mismatches 21; Indels 2; Gaps 1;
QY 2 DCSFQHSPTSSDFAVKIRELSYLLQDYFVTVASNLQDEELCGGLRWLVLAQRWVERLK 61
DB 30 DCSFQHSPTSSDFAVKIRELSYLLQDYFVTVASNLQDEELCGGLRWLVLAQRWVERLK 89
QY 62 VAGSKMQLLERNVTEIHFTVKAFQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 120
DB 90 VAGSKMQLLERNVTEIHFTVKAFQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 149
QY 121 QNFSRCLELOQCP 133
DB 150 QNFSRCLELOQCP 163
RESULT 5
I58343
flt3 ligand isoform SH - mouse
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
R;Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, I.
Oncogene 10, 143-157, 1995
A;Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand.
A;Reference number: I58343; MUID:95124710; PMID:7824267
A;Accession: I58343
A;Status: preliminary; translated from GB/EMBL/DDB3
A;Molecule type: mRNA
A;Residues: 1-220 <RES>
A;Cross-references: GB:S76459; NID:g913479; PID:AA333069.1; PID:g913480
Query Match 72.5%; Score 508; DB 2; Length 220;
Best Local Similarity 73.9%; Pred. No. 1.8e-45;
Matches 99; Conservative 12; Mismatches 21; Indels 2; Gaps 1;
QY 2 DCSFQHSPTSSDFAVKIRELSYLLQDYFVTVASNLQDEELCGGLRWLVLAQRWVERLK 61
DB 30 DCSFQHSPTSSDFAVKIRELSYLLQDYFVTVASNLQDEELCGGLRWLVLAQRWVERLK 89
QY 62 VAGSKMQLLERNVTEIHFTVKAFQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 120
DB 90 VAGSKMQLLERNVTEIHFTVKAFQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 149
QY 121 QNFSRCLELOQCP 133
DB 150 QNFSRCLELOQCP 163
RESULT 6
A49265
flt3/flk-2 ligand precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
R;Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holling
D.; Williams, D.E.; Beckmann, M.P.

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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:59:26 ; Search time 7.22826 Seconds

(without alignments)
958.091 Million cell updates/sec

Title: US-08-994-468-6_COPY_28_160

Perfect score: 701

Sequence: 1 QDCSFQHSPISSFAVKIRE.....LKPMWTRQNSRCLELQCP 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	701	100.0	235	1 FL3L HUMAN	P49771 homo sapien
2	508	72.5	232	1 FL3L MOUSE	P49772 mus musculus
3	78	77	205	1 CY8R-SYNY3	Q55854 synchocyst
4	78	11.1	872	1 SYR-HELPU	Q92661 helicobacte
5	75.5	10.8	301	1 KSGA-RICCN	Q92670 rickettsia
6	75	10.7	294	1 KSGA-STAAH	Q93291 staphylococ
7	75	10.7	297	1 KSGA-STAAH	Q99WB0 staphylococ
8	74.5	10.6	388	1 TRAG-BURCE	P24575 burkholderi
9	73	10.4	552	1 P52K-MOUSE	Q9CUX1 mus musculus
10	72.5	10.3	397	1 CERD-STRLC	P18549 streptomyc
11	72	10.3	362	1 OPRR-CHICK	P22329 gallus gali
12	71	10.1	341	1 PLSX-VIBCH	Q9KQH4 vibrio chol
13	71	10.1	661	1 AT12-VZVD	P09264 varicella-z
14	70.5	10.1	625	1 GLMS-SYNEL	Q8DJ16 s glucosami
15	70.5	10.1	1858	1 VGNB-CPSMV	P36312 cowpea seve
16	69.5	9.9	761	1 P52K-HUMAN	Q43422 homo sapien
17	69.5	9.9	1569	1 GLT3-XENLA	Q91660 xenopus lae
18	69	9.8	874	1 SYR-HELPU	P56000 helicobacte
19	68.5	9.8	426	1 B53B-HUMAN	Q94805 homo sapien
20	68.5	9.8	426	1 B53B-MOUSE	Q99MR0 mus musculus
21	68	9.7	566	1 TS13-MOUSE	Q01755 mus musculus
22	67.5	9.6	267	1 KSGA-BACTN	Q8A0H8 b dimethyla
23	67	9.6	446	1 TBTI-TRIVI	P31864 trichoderma
24	66.5	9.5	440	1 DGTI-VIBPA	Q87173 vibrio para
25	66.5	9.5	461	1 TM15-PIG	Q9TSW0 sus scrofa
26	66.5	9.5	497	1 RP54-PSEPK	P15591 pseudomonas
27	66.5	9.5	498	1 MEFA-MOUSE	Q60929 mus musculus
28	66	9.4	364	1 OPRR-HUMAN	P04000 homo sapien
29	66	9.4	439	1 VPF-EPMU	Q01259 bacterioph
30	66	9.4	805	1 KIP3-YEAST	P53086 saccharomyc
31	65.5	9.3	450	1 ROMA-RALSO	Q8Y035 raistonia s
32	65.5	9.3	467	1 YR72-ECOLI	P21312 escherichia
33	65.5	9.3	566	1 CRTI-ORYSA	Q9ZTN9 oryza sativ

ALIGNMENTS

RESULT 1

ID	FL3L HUMAN	STANDARD	PRT	235 AA
AC	P49771	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3L).			
GN	Flt3LG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OK	NCBI_TaxID=9606;			
NC	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=94195428; PubMed=8145851;			
RP	Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,			
RA	Bazan J.P., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,			
RA	Duda G., Martins N., Peterson D., Menon S., Shanafelt A.,			
RA	Muench M., Keiner G., Namikawa R., Rennick D., Roncarolo M.G.,			
RA	Zlotnik A., Kosmet O., Dubreuil P., Birnbaum D., Lee F.,			
RT	"Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of			
RT	haematopoietic stem cells and is encoded by variant RNAs."			
RL	Nature 368:643-648(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=94255842; PubMed=8180375;			
RX	Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,			
RX	Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.;			
RT	"Cloning of the human homologue of the murine flt3 ligand: a growth			
RT	factor for early hematopoietic progenitor cells."			
RL	Blood 83:2795-2801(1994).			
RL	[3]			
RN	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RP	MEDLINE=96032581; PubMed=7566977;			
RX	Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,			
RA	Escobar S.;			
RT	"Structural analysis of human and murine flt3 ligand genomic loci."			
RL	Oncogene 11:1165-1172(1995).			
RL	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).			
RX	MEDLINE=20343011; PubMed=10881197;			
RA	Savvides S.N., Boone T., Karplus P.A.;			
RT	"Flt3 ligand structure and unexpected commonalities of helical			
RT	bundles and cystine knots."			
RL	Nat. Struct. Biol. 7:486-491(2000).			
CC	!- FUNCTION: Stimulates the proliferation of early hematopoietic			
CC	cells. Synergizes well with a number of other colony stimulating			
CC	factors and interleukins.			
CC	!- SUBUNIT: Homodimer (isoform 2).			
CC	!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).			
CC	Secreted (isoform 2).			
CC	!- ALTERNATIVE PRODUCTS:			
CC	Event-Alternative splicing: Named isoforms=2;			
CC	Name=1; Synonyms=Membrane-bound;			

P49086 zea mays (m
Q14241 homo sapien
P44241 haemophilus
P34344 caenorhabdi
Q82d85 yersinia pe
P59157 s dimethyla
Q9ve01 drosofila
P54649 actinobacil
P71533 mycobacteri
Q14879 homo sapien
Q00416 saccharomyc
Q14517 homo sapien

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CC      isoid=p49771-1; Sequence=Displayed;
CC      Name=2; Synonyms=Soluble;
CC      isoid=p49771-2; Sequence=VSP_004251, VSP_004252;
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      -----
CC      EMBL; U04806; AAA17999.1; -
CC      EMBL; U03858; AAA19825.1; -
CC      EMBL; U29874; AAA90949.1; -
CC      EMBL; U29874; AAA90950.1; -
CC      PIR; I38440; I38440.
CC      PIR; I39076; I39076.
CC      PDB; 1ETE; 09-JUN-00.
CC      Genew; HGNC:3766; FLT3LG.
CC      MIN; 60007; -
CC      GO; GO:0005625; C:soluble fraction; TAS.
CC      GO; GO:0005102; F:receptor binding; TAS.
CC      GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
CC      GO; GO:0007185; P:signal transduction; TAS.
CC      InterPro; IPR004213; Flt3_lig.
CC      Pfam; PF02947; Flt3_lig; I.
CC      Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;
CC      3D-structure.
CC      SIGNAL      1      26
CC      CHAIN      27      235
CC      DOMAIN      27      184
CC      TRANSMEM      185      205
CC      DOMAIN      206      235
CC      DISULFID      30      111
CC      DISULFID      70      153
CC      DISULFID      119      158
CC      CARBOHYD      126      126
CC      CARBOHYD      149      149
CC      VARSPPLIC      161      178
CC
CC      179      235
CC      VARSPPLIC
CC      CONFLICT      72      72
CC      STRAND      31      31
CC      TURN      39      40
CC      HELIX      41      49
CC      TURN      50      51
CC      STRAND      53      53
CC      TURN      54      55
CC      STRAND      57      61
CC      STRAND      64      64
CC      TURN      68      70
CC      HELIX      71      87
CC      TURN      88      89
CC      STRAND      90      90
CC      HELIX      92      104
CC      HELIX      106      110
CC      TURN      118      119
CC      STRAND      122      126
CC      TURN      127      141
CC      TURN      142      147
CC      STRAND      149      149
CC      HELIX      151      153
CC      STRAND      158      158
CC      SEQUENCE      235 AA; 73B95BF693B4CECF CRC64;
CC
CC      Query Match      100.0%; Score 701; DB 1; Length 235;
CC      Best Local Similarity      100.0%; Pred. No. 8.1e-66;
CC      Matches 133; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
CC
CC      1 QDCSFQHSPISSDFAVKIRELSVLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
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Db      28 QDCSFQHSPISSDFAVKIRELSVLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 87
Qy      61 TVAGSKMGLLERNVTEHFVTKCAFOPPPSCLRPVQTNISRLLOETSEQLVALKPWITR 120
Db      88 TVAGSKMGLLERNVTEHFVTKCAFOPPPSCLRPVQTNISRLLOETSEQLVALKPWITR 147
Qy      121 QNFSRCLELQCOQ 133
Db      148 QNFSRCLELQCOQ 160

RESULT 2
FL3L MOUSE
ID FL3L MOUSE STANDARD; PRT; 232 AA.
AC P49772; Q64085;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SL cytokine precursor (fms-related tyrosine kinase 3 ligand) (Flt3
ligand) (Flt3L).
GN FLT3LG OR FLT3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=941195428; PubMed=8145851;
RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
RA Baza J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,
RA Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
RA Muench M., Kainer G., Namikawa R., Rennick D., Roncarolo M.G.,
RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
RT "Ligand for Flt3/Flk2 receptor tyrosine kinase regulates growth of
RT haematopoietic stem cells and is encoded by variant RNAs.";
RL Nature 368:643-648(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SJL/J;
RX MEDLINE=94084791; PubMed=7505204;
RA Lyman S.D., James L., Vanden Bos T., Devries P., Brasel K.,
RA Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
RA Splet R.R., Fletcher F.A., Maraskovsky E., Farrah T.,
RA Foxworth D., Williams D.E., Beckmann M.P.;
RT "Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
RT receptor: a proliferative factor for primitive hematopoietic cells.";
RL Cell 75:1157-1167(1993).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=96032581; PubMed=7566977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
RA Escobar S.;
RT "Structural analysis of human and murine flt3 ligand genomic loci.";
RL Oncogene 11:1165-1172(1995).
RN [4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=95124710; PubMed=7824267;
RA Lyman S.D., James L., Escobar S., Downey H., de Vries P.,
RA Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,
RA Cleveland L.S.;
RT "Identification of soluble and membrane-bound isoforms of the murine
RT flt3 ligand generated by alternative splicing of mRNAs.";
RL Oncogene 10:149-157(1995).
RN [5]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J.,
RA Franz-Bacon K., Mattson J., Tsai S., Luh J., Guimares M.J.,
RA Mattei M.-G., Rosnet O., Birnbaum D., Hannum C.;
RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Stimulates the proliferation of early hematopoietic
CC cells. Synergizes well with a number of other colony stimulating
CC factors and interleukins.
```

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OM protein - protein search, using sw model

Run on: April 8, 2004, 17:02:32 ; Search time 26.0217 Seconds
(without alignments)
1612.649 Million cell updates/sec

Title: US-08-994-468-6_COPY_28_160

Perfect score: 701

Sequence: 1 QDCSPQHSPISSDFAVKIRE.....LKPWITRONFSRCLSLQCOQ 133

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_25:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bactexiap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	683	97.4	236	6 Q86523	Q86523 papio cynoc
2	581	82.9	291	6 Q9M2U9	Q9m2u9 felis silve
3	581	82.9	294	6 Q9MZV0	Q9mzv0 canis famil
4	569	81.2	292	6 Q9GKE0	Q9gke0 bos taurus
5	569	81.2	292	6 Q8WVW1	Q8wvw1 bos taurus
6	508	72.5	172	11 Q61104	Q61104 mus musculu
7	481	68.6	169	11 Q8VCH4	Q8vch4 mus musculu
8	475	67.8	274	6 Q9GKD9	Q9gkd9 bos taurus
9	276	39.4	54	4 Q7Z6N5	Q7z6n5 homo sapien
10	79	11.3	497	13 Q80311	Q80311 brachydanio
11	79	11.3	1262	10 Q84KC6	Q84kc6 hordem vul
12	78	11.1	301	16 Q7WEM8	Q7wem8 bordetella
13	78	11.1	301	16 Q7W3A9	Q7w3a9 bordetella
14	78	11.1	301	16 Q7VU45	Q7vu45 bordetella
15	77.5	11.1	356	2 Q8KR32	Q8kr32 yersinia ps
16	77	11.0	1379	4 Q9P2D0	Q9p2d0 homo sapien

17	74.5	10.6	399	17	Q8PZ07	Q8p207 methanearc
18	74.5	10.6	505	5	Q86BP3	Q86bp3 drosophila
19	74.5	10.6	560	5	Q9V158	Q9v158 drosophila
20	74.5	10.6	990	5	Q86HM7	Q86hm7 dictyosteli
21	74.5	10.6	1188	17	Q57849	Q57849 pyrococcus
22	74	10.6	966	5	Q44066	Q44066 paraurostyl
23	74	10.6	1020	5	Q961A9	Q961a9 drosophila
24	74	10.6	1154	5	Q9VCW3	Q9vcw3 drosophila
25	74	10.6	1200	5	Q86PB8	Q86pb8 drosophila
26	73.5	10.5	506	16	Q83CR1	Q83cr1 coxiella bu
27	73	10.4	359	13	Q9W771	Q9w771 columba liv
28	73	10.4	758	11	Q80Y58	Q80y58 mus musculu
29	72.5	10.3	646	10	Q7XWT3	Q7xwt3 oryza sativ
30	72	10.3	2627	4	Q99773	Q99773 homo sapien
31	71.5	10.2	536	15	Q91E85	Q91e85 human immun
32	71.5	10.2	832	16	Q9XOV8	Q9xov8 thermotoga
33	71	10.1	431	12	Q9DW69	Q9dw69 rat cytomeg
34	71	10.1	561	10	Q81634	Q81634 elaeis olei
35	71	10.1	663	16	Q53649	Q53649 mycobacteri
36	71	10.1	663	16	Q7U2L2	Q7u2l2 mycobacteri
37	71	10.1	1085	10	Q9PFS5	Q9pfs5 arabidopsis
38	70.5	10.1	285	16	Q92DJ0	Q92dj0 listeria in
39	70.5	10.1	490	10	Q8GKX5	Q8gkx5 arabidopsis
40	70.5	10.1	499	10	Q9LX22	Q9lx22 arabidopsis
41	70	10.0	150	16	Q8DP35	Q8dp35 streptococc
42	70	10.0	298	16	Q7VE54	Q7ve54 prochlorococ
43	70	10.0	371	2	Q9F5P9	Q9f5p9 ectothiorho
44	70	10.0	438	16	Q8DC67	Q8dc67 vibrio vuln
45	70	10.0	553	16	Q9KC39	Q9kc39 bacillus ha

ALIGNMENTS

RESULT 1

Q86523 PRELIMINARY; PRT; 236 AA.
AC Q86523;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE FLT3 ligand.
OS Papio cynocephalus x Papio anubis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=208510;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalina T., Storek J.;
RT "T-cell reconstitution after autologous CD34 cell transplantation in
RT monkeys";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY226585; AA072538.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR InterPro; IPR004213; FIt3_lig.
DR Pfam; PF02947; FIt3_lig; I.
SQ SEQUENCE 236 AA; 26591 MW; 740F33A6A6DC2163 CRC64;

Query Match 97.4%; Score 683; DB 6; Length 236;

Best Local Similarity 97.7%; Pred. No. 5.9e-69;

Matches 130; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	QDCSPQHSPISSDFAVKIRELSYLLQDYPTVTSNQLQDEELCGGLWELVLAQSWNELK	60
DB	28	QDCSPQHSPISSDFAVKIRELSYLLQDYPTVTSNQLQDEELCGGLWELVLAQSWNELK	87
QY	61	TVASGKMGLLERVNTEIHFVTKAFOPPPSCAFVQTNISRLLOETSEQLVAKPWITR	120
DB	88	TVASGKMGLLERVNTEIHFVTKAFOPPPSCAFVQTNISRLLOETSEQLVAKPWITR	147
QY	121	QNFSRCLSLQCOQ	133

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DR InterPro; IPR004213; Flt3_lig.  
PFam; PF02947; flt3_lig; 1.  
SQ SEQUENCE   294 AA; 32394 MW; 68599917A3B74ABCD CRC64;  
  
Query Match      82.9%; Score 581; DB 6; Length 294;  
Best Local Similarity 84.1%; Pred.No. 2,6e-57;  
Matches 111; Conservative 7; Mismatches 14; Indels 0; Gaps 0;  
  
QY    2 DCSFHSPISDPFAVKIRELSYLQDYPTVTVASNLQDSEELCGGLWRLVLQAQRWMERLKT 61  
| | | | | | | | | | | | | | | | | | | | | : | | | | |  
Db    29 DCSFHSPISSFTAVIRKSLSYLLQDYPTVTVASNLDDELGCAGFWRLVLQAQRWMVRLOA 88  
| | | | | | | | | | | | | | | | | | | | | : | | | | |  
QY    62 VAGSNKGGLLERVNTEIHFVTSCAFPPPSCLRFVQTNISRLLOETSEOLVALKPWITRQ 121  
| | | | | | | | | | | | | | | | | | | | | : | | | | |  
Db    89 VAGSQNGILLEAVNTEIHFVTSCAFPLPSCFLRFVQTNIHSHLLQDTSSQLAAKPWITRR 148  
| | | | | | | | | | | | | | | | | | | | | : | | | | |  
QY    122 NFSRCLELCQP 133  
| | | | | | | | | | | | | | | | | | | | |  
Db    149 NFSGCELCQP 160  
| | | | | | | | | | | | | | | | | | | | |  
  
RESULT 4  
QSGKEO PRELIMINARY; PRT; 292 AA.  
ID ID QSGKEO AC  
Q9GKE0; AC  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Flt3 ligand isoform-1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=20570936; PubMed=11120823;  
RX Mwargi W., Brown W.C., Palmer G.H.;  
RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain  
required for receptor binding and function using naturally occurring  
ligand isoforms";  
RT J. Immunol. 185:6966-6974(2000).  
RL ENBL; AF282985; AAF9322.1; -.  
DR HSSP; P49771; IETE.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005125; F:cytokine activity; IEA.  
DR InterPro; IPR004213; Flt3_lig.  
DR Pfam; PF02947; flt3_lig; 1.  
DS SQ SEQUENCE   292 AA; 32390 MW; D68B9ED79221202D CRC64;  
  
Query Match      81.2%; Score 569; DB 6; Length 292;  
Best Local Similarity 81.1%; Pred.No. 6e-56;  
Matches 107; Conservative 10; Mismatches 15; Indels 0; Gaps 0;  
  
QY    2 DCSFHSPISDPFAVKIRELSYLQDYPTVTVASNLQDSEELCGGLWRLVLQAQRWMERLKT 61  
| | | | | | | | | | | | | | | | | | | | | : | | | | |  
Db    30 DCSFRHSPISSFTAKIKSLSYLQDYPTVTVASNLDDELGCAGFWRLVLQAQRWMGRCLK 89  
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QY    62 VAGSNKGGLLERVNTEIHFVTSCAFPPPSCLRFVQTNISRLLOETSEOLVALKPWITRQ 121  
| | | | | | | | | | | | | | | | | | | | | : | | | | |  
Db    90 VAGSEMEXLLEDVNTEIHFVTSCAFPLPSCFLRFVQANISHLLQTHQOLEALKPWITRR 149  
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QY    122 NFSRCLELCQP 133  
| | | | | | | | | | | | | | | | | | | | |  
Db    150 NFSRCLELCQP 161  
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RESULT 5  
QBWNWI PRELIMINARY; PRT; 292 AA.  
ID QBWNWI AC  
Q8WNW1; AC  
DT 01-NAR-2002 (TrEMBLrel. 20, Created)  
DT 01-NAR-2002 (TrEMBLrel. 20, Last sequence update)
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683.251 Million cell updates/sec

Perfect score: 701
Sequence: 1 QDCSFQHSPISSDPAVKIRE.....LKPWITRONFSRCLQLCCQP 133

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Post-processing: Minimum Match 100%

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1:  _ geneseq1980s:*
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3: geneseqp2000s:*

5: genesep2002s: *
6: genesepm2003as: *

6: geneseqp2003ab:*

References

Pred. No. is the number of results predicted by chance to have a

2000

Result No.	Score	Query		DB	ID	Description
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1	701	100.0	135	2	Aaw77910	Human flt
2	701	100.0	135	2	Aaw77912	Human flt
3	701	100.0	135	2	Aaw69034	Human flt
4	701	100.0	135	2	Aaw69036	Human flt
5	701	100.0	139	2	Aaw77782	Human flt
6	701	100.0	139	2	Aaw69006	Human flt
7	701	100.0	140	2	Aaw77911	Human flt
8	701	100.0	140	2	Aaw77913	Human flt
9	701	100.0	140	2	Aaw77908	Human flt
10	701	100.0	140	2	Aaw69032	Human flt
11	701	100.0	140	2	Aaw69035	Human flt
12	701	100.0	140	2	Aaw69037	Human flt
13	701	100.0	143	2	Aaw77926	Flt3 liga
14	701	100.0	143	2	Aaw69050	Human flt
15	701	100.0	144	2	Aaw77928	Flt3 liga
16	701	100.0	144	2	Aaw69052	Human flt
17	701	100.0	145	2	Aaw77925	Flt3 liga
18	701	100.0	145	2	Aaw69049	Human flt
19	701	100.0	149	2	Aaw77927	Flt3 liga
20	701	100.0	149	2	Aaw69051	Human flt
21	701	100.0	150	2	Aaw77930	Flt3 liga
22	701	100.0	150	2	Aaw69054	Human flt
23	701	100.0	153	2	Aaw77929	Flt3 liga
24	701	100.0	153	2	Aaw69053	Human flt
25	701	100.0	156	6	Abp72857	Human flt

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PR 25-OCT-1996; 96US-0029629P.
XX (SEAR ) SEARLE & CO G D.
XX McWherter CA, Feng Y, McKearn JP, Summers NL, Staten NR;
PI Streeter PR, Minnerly JC, Minster NI, Woulfe SL;
XX WPI; 1998-261504/23.
XX N-PSDB; AAV55203.
XX Multi-functional chimeric haematopoietic receptor agonist - useful to
PT treat haematopoietic disorders, tumours, infections or autoimmune
PT diseases.
XX Example 100; Page 206; 841pp; English.
XX Protein pMON32329.pgp is a human flt3 ligand encoded by plasmid
CC pMON32329 (see AAV55203), and is suitable for expression in Escherichia
CC coli. The invention relates to multi-functional chimeric haematopoietic
CC receptor agonists (see e.g. AAV7780-822) that may include flt3 receptor
CC agonists comprising sequence- rearranged flt3 ligand (see AAV7782).
CC These novel chimeric agonists can be used to stimulate the production of
CC haematopoietic cells in a patient, for the ex vivo expansion of
CC haematopoietic cells, for the production of dendritic cells and to treat
CC haematopoietic disorders, tumours, infection or autoimmune diseases
XX Sequence 135 AA;
SQ
Query Match 100.0%; Score 701; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.4e-76;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QDCSFQHSPISSDPAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
DB 3 QDCSFQHSPISSDPAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWMERLK 62
QY 61 TVAGSKMGGLERVNTIEHFVTKCAFQPPSCFLRFVQTNISRLLOETSEQLVAKPWITR 120
DB 63 TVAGSKMGGLERVNTIEHFVTKCAFQPPSCFLRFVQTNISRLLOETSEQLVAKPWITR 122
QY 121 QNFSRCLELCQP 133
DB 123 QNFSRCLELCQP 135
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AAW77912
ID AAW77912 standard; protein; 135 AA.
XX AC AAW77912;
XX 24-NOV-1998 (first entry)
XX Human flt3 ligand pMON32341.pgp.
XX Haematopoietic receptor agonist; flt3 receptor agonist; flt3 ligand;
KW human; chimeric protein; stem cell expansion; tumour; infection;
KW autoimmune disease; haematopoietic disorder; therapy; dendritic cell;
KW pMON32341.pgp.
XX Homo sapiens.
XX WO9817810-A2.
XX 30-APR-1998.
XX 23-OCT-1997; 97WO-US020037.
XX 25-OCT-1996; 96US-0029629P.
XX (SEAR ) SEARLE & CO G D.
XX McWherter CA, Feng Y, McKearn JP, Summers NL, Staten NR;
PI Streeter PR, Minnerly JC, Minster NI, Woulfe SL;
XX WPI; 1998-261504/23.
XX N-PSDB; AAV55203.
XX Multi-functional chimeric haematopoietic receptor agonist - useful to
PT treat haematopoietic disorders, tumours, infections or autoimmune
PT diseases.
XX Example 100; Page 206; 841pp; English.
XX Protein pMON32341.pgp is a human flt3 ligand encoded by plasmid
CC pMON32341 (see AAV55203), and is suitable for expression in Escherichia
CC coli. The invention relates to multi-functional chimeric haematopoietic
CC receptor agonists (see e.g. AAV7780-822) that may include flt3 receptor
CC agonists comprising sequence- rearranged flt3 ligand (see AAV7782).
CC These novel chimeric agonists can be used to stimulate the production of
CC haematopoietic cells in a patient, for the ex vivo expansion of
CC haematopoietic cells, for the production of dendritic cells and to treat
CC haematopoietic disorders, tumours, infection or autoimmune diseases
XX Sequence 135 AA;
SQ
Query Match 100.0%; Score 701; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.4e-76;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QDCSFQHSPISSDPAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
DB 3 QDCSFQHSPISSDPAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWMERLK 62
QY 61 TVAGSKMGGLERVNTIEHFVTKCAFQPPSCFLRFVQTNISRLLOETSEQLVAKPWITR 120
DB 63 TVAGSKMGGLERVNTIEHFVTKCAFQPPSCFLRFVQTNISRLLOETSEQLVAKPWITR 122
QY 121 QNFSRCLELCQP 133
DB 123 QNFSRCLELCQP 135
RESULT 3
AAW69034
ID AAW69034 standard; protein; 135 AA.
XX AC AAW69034;
XX 01-OCT-1998 (first entry)
XX Human flt-3 receptor agonist pMON32329.pgp.
XX Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer;
KW bone marrow reconstitution; haematological disease; immune deficiency;
KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;
KW congenital metabolic disease; neurological disease; therapy;
KW dendritic cell production.
XX Homo sapiens.
XX WO9818923-A1.
XX 07-MAY-1998.
XX 23-OCT-1997; 97WO-US018700.
XX 25-OCT-1996; 96US-0030094P.
XX (SEAR ) SEARLE & CO G D.
XX McWherter CA, Feng Y, McKearn JP, Staten NR, Streeter PR;
PI Woulfe SL, Minster NI, Minnerly JC;
XX WPI; 1998-272218/24.
XX N-PSDB; AAV69034.

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PI Streeter PR, Minnerly JC, Minster NI, Woulfe SL;
XX WPI; 1998-261504/23.
XX N-PSDB; AAV55203.
XX Multi-functional chimeric haematopoietic receptor agonist - useful to
PT treat haematopoietic disorders, tumours, infections or autoimmune
PT diseases.
XX Example 100; Page 206; 841pp; English.
XX Protein pMON32341.pgp is a human flt3 ligand encoded by plasmid
CC pMON32341 (see AAV55203), and is suitable for expression in Escherichia
CC coli. The invention relates to multi-functional chimeric haematopoietic
CC receptor agonists (see e.g. AAV7780-822) that may include flt3 receptor
CC agonists comprising sequence- rearranged flt3 ligand (see AAV7782).
CC These novel chimeric agonists can be used to stimulate the production of
CC haematopoietic cells in a patient, for the ex vivo expansion of
CC haematopoietic cells, for the production of dendritic cells and to treat
CC haematopoietic disorders, tumours, infection or autoimmune diseases
XX Sequence 135 AA;
SQ
Query Match 100.0%; Score 701; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.4e-76;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QDCSFQHSPISSDPAVKIRELSYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
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QY 61 TVAGSKMGGLERVNTIEHFVTKCAFQPPSCFLRFVQTNISRLLOETSEQLVAKPWITR 120
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ID AAW69034 standard; protein; 135 AA.
XX AC AAW69034;
XX 01-OCT-1998 (first entry)
XX Human flt-3 receptor agonist pMON32329.pgp.
XX Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer;
KW bone marrow reconstitution; haematological disease; immune deficiency;
KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;
KW congenital metabolic disease; neurological disease; therapy;
KW dendritic cell production.
XX Homo sapiens.
XX WO9818923-A1.
XX 07-MAY-1998.
XX 23-OCT-1997; 97WO-US018700.
XX 25-OCT-1996; 96US-0030094P.
XX (SEAR ) SEARLE & CO G D.
XX McWherter CA, Feng Y, McKearn JP, Staten NR, Streeter PR;
PI Woulfe SL, Minster NI, Minnerly JC;
XX WPI; 1998-272218/24.
XX N-PSDB; AAV69034.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 17:07:57 ; Search time 26.7446 Seconds
(without alignments)
1307.583 Million cell updates/sec

Title: US-08-994-468-6_COPY_28_160

Perfect score: 701

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	701	100.0	156	14	US-10-053-355A-1
2	701	100.0	209	9	US-09-904-536-11
3	701	100.0	212	9	US-09-904-536-10
4	701	100.0	235	8	US-08-994-468-6
5	701	100.0	235	9	US-09-448-378-1
6	701	100.0	235	9	US-09-983-806-6
7	701	100.0	235	9	US-09-904-536-1
8	701	100.0	235	12	US-10-643-384-2
9	701	100.0	235	13	US-10-095-449-6
10	701	100.0	235	14	US-10-241-927-2
11	701	100.0	235	14	US-10-314-035-6
12	701	100.0	235	16	US-10-401-364-1
13	697	99.4	209	9	US-09-904-536-9
14	697	99.4	209	9	US-09-904-536-12
15	697	99.4	209	9	US-09-904-536-14

16	697	99.4	209	9	US-09-904-536-17	Sequence 17, Appl
17	695	99.1	209	9	US-09-904-536-11	Sequence 11, Appl
18	695	99.1	209	9	US-09-904-536-15	Sequence 15, Appl
19	695	99.1	235	15	US-10-116-275-174	Sequence 174, Appl
20	695	99.1	235	15	US-10-440-464-60	Sequence 60, Appl
21	694	99.0	209	9	US-09-904-536-13	Sequence 13, Appl
22	693	98.9	209	9	US-09-904-536-8	Sequence 8, Appl
23	687	98.0	209	9	US-09-904-536-16	Sequence 16, Appl
24	581	82.9	265	14	US-10-218-654-49	Sequence 49, Appl
25	581	82.9	265	14	US-10-262-439-49	Sequence 49, Appl
26	581	82.9	268	14	US-10-218-654-23	Sequence 23, Appl
27	581	82.9	268	14	US-10-262-439-23	Sequence 23, Appl
28	581	82.9	291	14	US-10-218-654-44	Sequence 44, Appl
29	581	82.9	291	14	US-10-262-439-44	Sequence 44, Appl
30	581	82.9	294	14	US-10-218-654-7	Sequence 7, Appl
31	581	82.9	294	14	US-10-262-439-7	Sequence 7, Appl
32	508	72.5	231	8	US-08-994-468-2	Sequence 2, Appl
33	508	72.5	231	9	US-09-448-378-2	Sequence 2, Appl
34	508	72.5	231	9	US-09-983-806-2	Sequence 2, Appl
35	508	72.5	231	13	US-10-095-449-2	Sequence 2, Appl
36	508	72.5	231	14	US-10-314-035-2	Sequence 2, Appl
37	508	72.5	231	16	US-10-401-364-2	Sequence 2, Appl
38	502.5	71.7	137	9	US-09-904-536-19	Sequence 19, Appl
39	482	68.8	250	14	US-10-218-654-31	Sequence 31, Appl
40	482	68.8	250	14	US-10-262-439-31	Sequence 31, Appl
41	482	68.8	276	14	US-10-218-654-26	Sequence 26, Appl
42	482	68.8	276	14	US-10-262-439-26	Sequence 26, Appl
43	77	11.0	345	12	US-10-335-977-7085	Sequence 7085, Ap
44	77	11.0	535	12	US-10-335-977-7086	Sequence 7086, Ap
45	77	11.0	872	9	US-09-615-242-11563	Sequence 11563, A

ALIGNMENTS

RESULT 1
US-10-053-355A-1
; Sequence 1, Application US/10053355A
; Publication No. US20030077824A1
; GENERAL INFORMATION:
; APPLICANT: Rossi, Alex
; TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High Th
; FILE REFERENCE: A-70882/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/053,355A
; CURRENT FILING DATE: 2002-06-18
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-053-355A-1

Query Match 100.0%; Score 701; DB 14; Length 156;
Best Local Similarity 100.0%; Pred. No. 2e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QDCSFQHSPISSDFAVKIRELSDYLLQDPYVTVASNLQDEELCGGLWRLVLAQRWVERLK 60
DB 3 QDCSFQHSPISSDFAVKIRELSDYLLQDPYVTVASNLQDEELCGGLWRLVLAQRWVERLK 62
QY 61 TVAGSMQGLLRVNTETHFVTKCAFPQPPCLRVQTNISLLQETSEQLVAKPWITR 120
DB 63 TVAGSMQGLLRVNTETHFVTKCAFPQPPCLRVQTNISLLQETSEQLVAKPWITR 122
QY 121 QNFSRCLELQCCP 133
DB 123 QNFSRCLELQCCP 135

RESULT 2

US-09-904-536-18
; Sequence 18, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-18

Query Match 100.0%; Score 701; DB 9; Length 209;
Best Local Similarity 100.0%; Pred. No. 2.9e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDPFAVKIRELSYLLQDYFVTVASNLQDEELCGGLWRLVLAQRWNERLK 60
DB 2 QDCSFQHSPISSDPFAVKIRELSYLLQDYFVTVASNLQDEELCGGLWRLVLAQRWNERLK 61
QY 61 TVAGSKMQGLLERVNTTEIHFTVKCAFPQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 120
DB 62 TVAGSKMQGLLERVNTTEIHFTVKCAFPQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 121
QY 121 QNFSRCLELOCQP 133
DB 122 QNFSRCLELOCQP 134

RESULT 3

US-09-904-536-10
; Sequence 10, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-10

Query Match 100.0%; Score 701; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.9e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDPFAVKIRELSYLLQDYFVTVASNLQDEELCGGLWRLVLAQRWNERLK 60
DB 5 QDCSFQHSPISSDPFAVKIRELSYLLQDYFVTVASNLQDEELCGGLWRLVLAQRWNERLK 64
QY 61 TVAGSKMQGLLERVNTTEIHFTVKCAFPQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 120
DB 65 TVAGSKMQGLLERVNTTEIHFTVKCAFPQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 124
QY 121 QNFSRCLELOCQP 133

Db

125 QNFSRCLELOCQP 137

RESULT 4

US-08-994-468-6
; Sequence 6, Application US/08994468
; Publication No. US20030148516A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,468
; FILING DATE: 19-Dec-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,407
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-994-468-6

Query Match 100.0%; Score 701; DB 8; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDPFAVKIRELSYLLQDYFVTVASNLQDEELCGGLWRLVLAQRWNERLK 60
DB 28 QDCSFQHSPISSDPFAVKIRELSYLLQDYFVTVASNLQDEELCGGLWRLVLAQRWNERLK 87
QY 61 TVAGSKMQGLLERVNTTEIHFTVKCAFPQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 120
DB 88 TVAGSKMQGLLERVNTTEIHFTVKCAFPQPPSCILRFVQTNISRLLOETSEQLVALKPWITR 147
QY 121 QNFSRCLELOCQP 133
DB 148 QNFSRCLELOCQP 160

RESULT 5

US-09-448-378-1

```
; Sequence 1, Application US/09448378
; Patent No. US20020034517A1
; GENERAL INFORMATION:
; APPLICANT: Brasel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; - CURRENT APPLICATION NUMBER: US/09/448,378
; - CURRENT FILING DATE: 1999-11-23
; - NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-448-378-1

Query Match      100.0%; Score 701; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
Db 28 QDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 87
QY 61 TVAGSKMOGLLERVNTIHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 120
Db 88 TVAGSKMOGLLERVNTIHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 147
QY 121 QNFSRCLELQCCP 133
Db 148 QNFSRCLELQCCP 160

RESULT 6
US-09-983-806-6
; Sequence 6, Application US/09983806
; Patent No. US20020107365A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/983,806
; FILING DATE: 25-Oct-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,626
; FILING DATE: 19-May-1995
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C

; Sequence 1, Application US/09448378
; Patent No. US20020034517A1
; GENERAL INFORMATION:
; APPLICANT: Brasel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; - CURRENT APPLICATION NUMBER: US/09/448,378
; - CURRENT FILING DATE: 1999-11-23
; - NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-448-378-1

Query Match      100.0%; Score 701; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
Db 28 QDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 87
QY 61 TVAGSKMOGLLERVNTIHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 120
Db 88 TVAGSKMOGLLERVNTIHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 147
QY 121 QNFSRCLELQCCP 133
Db 148 QNFSRCLELQCCP 160

RESULT 7
US-09-904-536-1
; Sequence 1, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; Applicant: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-1

Query Match      100.0%; Score 701; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
Db 28 QDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 87
QY 61 TVAGSKMOGLLERVNTIHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 120
Db 88 TVAGSKMOGLLERVNTIHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 147
QY 121 QNFSRCLELQCCP 133
Db 148 QNFSRCLELQCCP 160

RESULT 8
US-10-643-384-2
; Sequence 2, Application US/10643384
; Publication No. US20040037845A1
; GENERAL INFORMATION:
```

APPLICANT: Brasel, Kenneth A.
APPLICANT: Lyman, Stewart D.
APPLICANT: Maraskovsky, Eugene
APPLICANT: McKenna, Hilary J.
APPLICANT: Lynch, David H.
TITLE OF INVENTION: THE USE OF FLT3-LIGAND IN THE TREATMENT OF INFECTION
FILE REFERENCE: 2836-F
CURRENT APPLICATION NUMBER: US/10/643,384
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: 10/241,927
PRIOR FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: 09/444,027
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 09/154,903
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 08/725,540
PRIOR FILING DATE: 1996-10-03
PRIOR APPLICATION NUMBER: 08/539,142
PRIOR FILING DATE: 1995-10-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-10-643-384-2

Query Match 100.0%; Score 701; DB 12; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDPAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWVERLK 60
DB 28 QDCSFQHSPISSDPAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWVERLK 87

QY 61 TVAGSKMGLLERNVTEIHFVTKAFOPPPSCFLRFVQTNISRLLOETSEQLVAKPWITR 120
DB 88 TVAGSKMGLLERNVTEIHFVTKAFOPPPSCFLRFVQTNISRLLOETSEQLVAKPWITR 147

QY 121 QNFSRCLELQCP 133
DB 148 QNFSRCLELQCP 160

RESULT 9
US-10-095-449-6
Sequence 6, Application US/10095449
Publication No. US20020160004A1
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,449
FILING DATE: 13-Mar-2002
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,692
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: US/08/162,407

FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-095-449-6

Query Match 100.0%; Score 701; DB 13; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDPAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWVERLK 60
DB 28 QDCSFQHSPISSDPAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWVERLK 87

QY 61 TVAGSKMGLLERNVTEIHFVTKAFOPPPSCFLRFVQTNISRLLOETSEQLVAKPWITR 120
DB 88 TVAGSKMGLLERNVTEIHFVTKAFOPPPSCFLRFVQTNISRLLOETSEQLVAKPWITR 147

QY 121 QNFSRCLELQCP 133
DB 148 QNFSRCLELQCP 160

RESULT 10
US-10-241-927-2
Sequence 2, Application US/10241927
Publication No. US20030113341A1
GENERAL INFORMATION:
APPLICANT: Lynch, David H.
APPLICANT: Borges, Luis
APPLICANT: Miller, Robert E.
APPLICANT: Maliszewski, Charles R.
TITLE OF INVENTION: THE USE OF FLT3-LIGAND IN THE TREATMENT OF CANCER
FILE REFERENCE: 2836-F
CURRENT APPLICATION NUMBER: US/10/241,927
CURRENT FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: US 09/444,027
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: US 09/154,903
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US 08/725,540
PRIOR FILING DATE: 1996-10-03
PRIOR APPLICATION NUMBER: US 08/539,142
PRIOR FILING DATE: 1995-10-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 235
TYPE: PRT
ORGANISM: homo sapiens
US-10-241-927-2

Query Match 100.0%; Score 701; DB 14; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVTASNLODEELCGGLWRLVLAQRWMERLK 60
D6 28 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVTASNLODEELCGGLWRLVLAQRWMERLK 87
QY 61 TVAGSKMQGLLERVNTTEHFVTKAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 120
D6 88 TVAGSKMQGLLERVNTTEHFVTKAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 147
QY 121 QNFSRCLELQCCP 133
D6 148 QNFSRCLELQCCP 160

RESULT 11
US-10-314-035-6
; Sequence 6, Application US/10314035
; Publication No. US20030157069A1
; GENERAL INFORMATION:
; APPLICANT: LYMAN, Stewart D.
; TITLE OF INVENTION: METHODS OF USING FLT3-LIGAND IN HEMATOPOIETIC CELL TRANSPLANTATION
; FILE REFERENCE: 2813-P
; CURRENT APPLICATION NUMBER: US/10/314,035
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US 08/994,468
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: US 08/444,627
; PRIOR FILING DATE: 1995-05-19
; PRIOR APPLICATION NUMBER: US 08/243,545
; PRIOR FILING DATE: 1994-05-11
; PRIOR APPLICATION NUMBER: US 08/209,502
; PRIOR FILING DATE: 1994-03-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-035-6

Query Match 100.0%; Score 701; DB 14; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVTASNLODEELCGGLWRLVLAQRWMERLK 60
D6 28 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVTASNLODEELCGGLWRLVLAQRWMERLK 87
QY 61 TVAGSKMQGLLERVNTTEHFVTKAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 120
D6 88 TVAGSKMQGLLERVNTTEHFVTKAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 147
QY 121 QNFSRCLELQCCP 133
D6 148 QNFSRCLELQCCP 160

RESULT 12
US-10-401-364-1
; Sequence 1, Application US/10401364
; Publication No. US20040022760A1
; GENERAL INFORMATION:
; APPLICANT: McKenna, Hilary J.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Maliszewski, Charles R.
; TITLE OF INVENTION: METHODS OF USING FLT3-LIGAND IN IMMUNIZATION PROTOCOLS
; FILE REFERENCE: 3399-B
; CURRENT APPLICATION NUMBER: US/10/401,364
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US 60/368,263
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/427,835

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; PRIOR FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-364-1

Query Match 100.0%; Score 701; DB 16; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVTASNLODEELCGGLWRLVLAQRWMERLK 60
D6 28 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVTASNLODEELCGGLWRLVLAQRWMERLK 87
QY 61 TVAGSKMQGLLERVNTTEHFVTKAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 120
D6 88 TVAGSKMQGLLERVNTTEHFVTKAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 147
QY 121 QNFSRCLELQCCP 133
D6 148 QNFSRCLELQCCP 160

RESULT 13
US-09-904-536-9
; Sequence 9, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-9

Query Match 99.4%; Score 697; DB 9; Length 209;
Best Local Similarity 99.2%; Pred. No. 8.5e-74;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVTASNLODEELCGGLWRLVLAQRWMERLK 60
D6 2 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVTASNLODEELCGGLWRLVLAQRWMERLK 61
QY 61 TVAGSKMQGLLERVNTTEHFVTKAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 120
D6 62 TVAGSKMQGLLERVNTTEHFVTKAFQPPPSCLRFVQTNISRLLOETSEQLVALKPWITR 121
QY 121 QNFSRCLELQCCP 133
D6 122 QNFSRCLELQCCP 134

RESULT 14
US-09-904-536-12
; Sequence 12, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028

```

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; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-12

Query Match          99.4%; Score 697; DB 9; Length 209;
Best Local Similarity 99.2%; Pred. No. 8.5e-74;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QDCSFQHSPISSDFAVKIRELSDYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
Db      1 QDCSFQHSPISSDFAVKIRELSDYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWMERLK 61

QY      61 TVAGSKMQGLLERVNTIEHFVTKCAFPQPPSCILRFVQTNISRLQETSEQLVALKPWITR 120
Db      61 TVAGSKMQGLLERVNTIEHFVTKCAFPQPPSCILRFVQTNISRLQETSEQLVALKPWITR 121

QY      121 QNFSRCLELQCCP 133
Db      121 QNFSRCLELQCCP 134

RESULT 15
US-09-904-536-14
; Sequence 14, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-14

Query Match          99.4%; Score 697; DB 9; Length 209;
Best Local Similarity 99.2%; Pred. No. 8.5e-74;
Matches 132; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 QDCSFQHSPISSDFAVKIRELSDYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
Db      1 QDCSFQHSPISSDFAVKIRELSDYLLQDYPTVTVASNLQDEELCGGLWRLVLAQRWMERLK 61

QY      61 TVAGSKMQGLLERVNTIEHFVTKCAFPQPPSCILRFVQTNISRLQETSEQLVALKPWITR 120
Db      61 TVAGSKMQGLLERVNTIEHFVTKCAFPQPPSCILRFVQTNISRLQETSEQLVALKPWITR 121

QY      121 QNFSRCLELQCCP 133
Db      121 QNFSRCLELQCCP 134
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Search completed: April 8, 2004, 17:17:21
JOB time : 27.7446 SECS

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 17:03:57 ; Search time 11.9266 Seconds
(without alignments)
575.708 Million cell updates/sec

Title: US-08-994-468-6_COPY_28_160

Perfect score: 701
Sequence: 1 QDCSFQHSPISSDFAVKIRE.....LKPWTRQNSRCLELOQCP 133

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
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5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	701	100.0	209	3	US-09-109-100-18
2	701	100.0	212	3	US-09-109-100-10
3	701	100.0	235	1	US-08-243-545-6
4	701	100.0	235	2	US-08-993-962-6
5	701	100.0	235	3	US-09-160-841-6
6	701	100.0	235	3	US-09-109-100-1
7	701	100.0	235	4	US-08-669-692-6
8	701	100.0	235	4	US-08-444-526-6
9	701	100.0	235	5	PCT-US94-05365-6
10	697	99.4	209	3	US-09-109-100-9
11	697	99.4	209	3	US-09-109-100-12
12	697	99.4	209	3	US-09-109-100-14
13	697	99.4	209	3	US-09-109-100-17
14	695	99.1	209	3	US-09-109-100-11
15	695	99.1	209	3	US-09-109-100-15
16	694	99.0	209	3	US-09-109-100-13
17	693	98.9	209	3	US-09-109-100-8
18	687	98.0	209	3	US-09-109-100-16
19	581	82.9	265	4	US-09-322-409-49
20	581	82.9	265	4	US-09-451-527-49
21	581	82.9	268	4	US-09-322-409-23
22	581	82.9	268	4	US-09-451-527-23
23	581	82.9	291	4	US-09-322-409-44
24	581	82.9	291	4	US-09-451-527-44
25	581	82.9	294	4	US-09-322-409-7
26	581	82.9	294	4	US-09-451-527-7
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28 508 72.5 231 1 US-08-243-545-2 Sequence 2, Appli
29 508 72.5 231 2 US-08-993-962-2 Sequence 2, Appli
30 508 72.5 231 3 US-09-160-841-2 Sequence 2, Appli
31 508 72.5 231 4 US-08-669-692-2 Sequence 2, Appli
32 508 72.5 231 5 US-08-444-626-2 Sequence 2, Appli
33 508 72.5 231 5 PCT-US94-05365-2 Sequence 2, Appli
34 508 72.5 231 5 PCT-US95-03866-6 Sequence 6, Appli
35 502.5 71.7 137 3 US-09-109-100-19 Sequence 19, Appli
36 482 68.8 250 4 US-09-322-409-31 Sequence 31, Appli
37 482 68.8 250 4 US-09-451-527-31 Sequence 31, Appli
38 482 68.8 276 4 US-09-322-409-26 Sequence 26, Appli
39 482 68.8 276 4 US-09-451-527-26 Sequence 26, Appli
40 150 21.4 42 5 PCT-US94-05150-17 Sequence 17, Appli
41 79.5 11.3 2618 3 US-09-413-814-28 Sequence 28, Appli
42 79 11.3 28 5 PCT-US94-05150-12 Sequence 12, Appli
43 71 10.1 22 5 PCT-US94-05150-10 Sequence 10, Appli
44 70.5 10.1 873 2 US-08-912-129A-61 Sequence 61, Appli
45 69 9.8 872 1 US-08-451-715A-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-109-100-18
; Sequence 18, Application US/09109100C
; Patent No. 6291861
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-18

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Best Local Similarity 100.0%; Pred. No. 5.6e-80;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 2 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNIQDELCGLRLVLAQRMWERLK 61
QY 61 TVAGSKMGLLERYNTEIHFVTKCAFQPPSPCLFVQTNISRLLOETSEQLVAKPWITR 120
DB 62 TVAGSKMGLLERYNTEIHFVTKCAFQPPSPCLFVQTNISRLLOETSEQLVAKPWITR 121

QY 121 QNFSRCLELOQCP 133
DB 122 QNFSRCLELOQCP 134
RESULT 2
US-09-109-100-10
; Sequence 10, Application US/09109100C
; Patent No. 6231661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10

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; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-10

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Best Local Similarity 100.0%; Pred. No. 5.7e-80;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TVAGSMQGLLRRVNTIHFVTKCAFQPPPPCLRFVQTNISRLQETSEQLVALKPWITR 120
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QY 121 QNFSRCLELQCOQ 133
Db 125 QNFSRCLELQCOQ 137

RESULT 3
US-08-243-545-6
; Sequence 6, Application US/08243545
; Patent No. 5554512
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,545
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-243-545-6

Query Match      100.0%; Score 701; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 6.6e-80;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TVAGSMQGLLRRVNTIHFVTKCAFQPPPPCLRFVQTNISRLQETSEQLVALKPWITR 120
Db 88 TVAGSMQGLLRRVNTIHFVTKCAFQPPPPCLRFVQTNISRLQETSEQLVALKPWITR 147
QY 121 QNFSRCLELQCOQ 133
Db 148 QNFSRCLELQCOQ 160

RESULT 4
US-08-993-962-6
; Sequence 6, Application US/08993962
; Patent No. 5843423
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,962
; FILING DATE: December 18, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: Protein
US-08-993-962-6
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Best Local Similarity 100.0%; Pred. No. 6.6e-80;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 28 QDCSFQHSPISSDFAVKIRELSVLLQDYPTVASNLQDEELCGGLWRLVLAQRWMERLK 87

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QY 121 QNFSRCLELOQCP 133
Db 148 QNFSRCLELOQCP 160

RESULT 5
US-09-160-841-6
; Sequence 6, Application US/09160841
; Patent No. 6190655
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation.
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-160-841-6
Query Match      100.0%; Score 701; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 6.6e-80;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSVLLQDYPTVASNLQDEELCGGLWRLVLAQRWMERLK 60
Db 28 QDCSFQHSPISSDFAVKIRELSVLLQDYPTVASNLQDEELCGGLWRLVLAQRWMERLK 87

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Db 88 TVAGSKMQGLLERVNTIHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 147

QY 121 QNFSRCLELOQCP 133
Db 148 QNFSRCLELOQCP 160

RESULT 6
US-09-109-100-1
; Sequence 1, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-1
Query Match      100.0%; Score 701; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 6.6e-80;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSVLLQDYPTVASNLQDEELCGGLWRLVLAQRWMERLK 60
Db 28 QDCSFQHSPISSDFAVKIRELSVLLQDYPTVASNLQDEELCGGLWRLVLAQRWMERLK 87

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Db 88 TVAGSKMQGLLERVNTIHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 147

QY 121 QNFSRCLELOQCP 133
Db 148 QNFSRCLELOQCP 160

RESULT 7
US-08-669-692-6
; Sequence 6, Application US/08669692
; Patent No. 6630143
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,692
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-669-692-6

Query Match 100.0%; Score 701; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 6.6e-80;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSFISDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRMWRLK 60
DB 28 QDCSFQHSFISDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRMWRLK 87
QY 61 TVAGSKMOGLLERNVTEIHFTVKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 120
DB 88 TVAGSKMOGLLERNVTEIHFTVKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 147
QY 121 QNFSRCLELQCOQ 133
DB 148 QNFSRCLELQCOQ 160

RESULT 8
US-08-444-626-6
; Sequence 6, Application US/08444626
; Patent No. 632424
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,626
; FILING DATE: 19-MAY-1995

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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-626-6

Query Match 100.0%; Score 701; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 6.6e-80;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSFISDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRMWRLK 60
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QY 61 TVAGSKMOGLLERNVTEIHFTVKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 120
DB 88 TVAGSKMOGLLERNVTEIHFTVKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 147
QY 121 QNFSRCLELQCOQ 133
DB 148 QNFSRCLELQCOQ 160

RESULT 9
PCI-US94-05365-6
; Sequence 6, Application PC/TUS9405365
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05365
; FILING DATE: May 24, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: -to be assigned-

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FILING DATE: May 11, 1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/209,502
 FILING DATE: March 7, 1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/162,407
 FILING DATE: December 3, 1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/111,758
 FILING DATE: August 25, 1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/106,463
 FILING DATE: August 12, 1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/068,394
 FILING DATE: May 24, 1993
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Malaska, Stephen L.
 REGISTRATION NUMBER: 32,655
 REFERENCE/DOCKET NUMBER: 2813-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 235 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US94-05365-6

Query Match 100.0%; Score 701; DB 5; Length 235;
 Best Local Similarity 100.0%; Pred. No. 6.6e-80;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWRLK 60
 Db 28 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWRLK 87
 QY 61 TVAGSKMOGLLERNVTEHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 120
 Db 88 TVAGSKMOGLLERNVTEHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 147
 QY 121 QNFSRCLELQCOQ 133
 Db 148 QNFSRCLELQCOQ 160

RESULT 10
 US-09-109-100-9
 ; Sequence 9, Application US/09109100C
 ; Patent No. 6291661
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/109,100C
 ; CURRENT FILING DATE: 1998-07-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-109-100-9

Query Match 99.4%; Score 697; DB 3; Length 209;
 Best Local Similarity 99.2%; Pred. No. 1.8e-79;
 Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWRLK 60
 Db 2 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWRLK 61
 QY 61 TVAGSKMOGLLERNVTEHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 120
 Db 62 TVTGSKMQGLLERNVTEHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 121
 QY 121 QNFSRCLELQCOQ 133
 Db 122 QNFSRCLELQCOQ 134

RESULT 11
 US-09-109-100-12
 ; Sequence 12, Application US/09109100C
 ; Patent No. 6291661
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/109,100C
 ; CURRENT FILING DATE: 1998-07-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-109-100-12

Query Match 99.4%; Score 697; DB 3; Length 209;
 Best Local Similarity 99.2%; Pred. No. 1.8e-79;
 Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWRLK 60
 Db 2 QDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLWRLVLAQRWRLK 61
 QY 61 TVAGSKMOGLLERNVTEHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 120
 Db 62 TVAGSKMOGLLERNVTEHFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVAKPWITR 121
 QY 121 QNFSRCLELQCOQ 133
 Db 122 QNFSRCLELQCOQ 134

RESULT 12
 US-09-109-100-14
 ; Sequence 14, Application US/09109100C
 ; Patent No. 6291661
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/109,100C
 ; CURRENT FILING DATE: 1998-07-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-109-100-14

Query Match 99.4%; Score 697; DB 3; Length 209;
Best Local Similarity 99.2%; Pred. No. 1.8e-79;
Matches 132; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
DB 2 QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 61

QY 61 TVAGSKMOGLLERVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWITR 120
DB 62 TVAGSKMOGLLERVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWITR 121

QY 121 QNFSRCLELQCP 133
DB 122 QNFSRCLELQCP 134

RESULT 13
US-09-109-100-17
; Sequence 17, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-17

Query Match 99.4%; Score 697; DB 3; Length 209;
Best Local Similarity 99.2%; Pred. No. 1.8e-79;
Matches 132; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
DB 2 QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 61

QY 61 TVAGSKMOGLLERVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWITR 120
DB 62 TVAGSKMOGLLERVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWITR 121

QY 121 QNFSRCLELQCP 133
DB 122 QNFSRCLELQCP 134

RESULT 14
US-09-109-100-11
; Sequence 11, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-11

Query Match 99.1%; Score 695; DB 3; Length 209;

Best Local Similarity 99.2%; Pred. No. 3.2e-79;
Matches 132; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
DB 2 QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 61

QY 61 TVAGSKMOGLLERVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWITR 120
DB 62 TVAGSKMOGLLERVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWITR 121

QY 121 QNFSRCLELQCP 133
DB 122 QNFSRCLELQCP 134

RESULT 15
US-09-109-100-15
; Sequence 15, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-15

Query Match 99.1%; Score 695; DB 3; Length 209;
Best Local Similarity 99.2%; Pred. No. 3.2e-79;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 60
DB 2 QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLK 61

QY 61 TVAGSKMOGLLERVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWITR 120
DB 62 TVAGSKMOGLLERVNTIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWITR 121

QY 121 QNFSRCLELQCP 133
DB 122 QNFSRCLELQCP 134

Search completed: April 8, 2004, 17:09:12
Job time : 12.9266 secs